



results of BLAST

BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1109098562-18357-122032509583.BLASTQ2

Query=

(378 letters)

SEQ ID NO: 2

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples

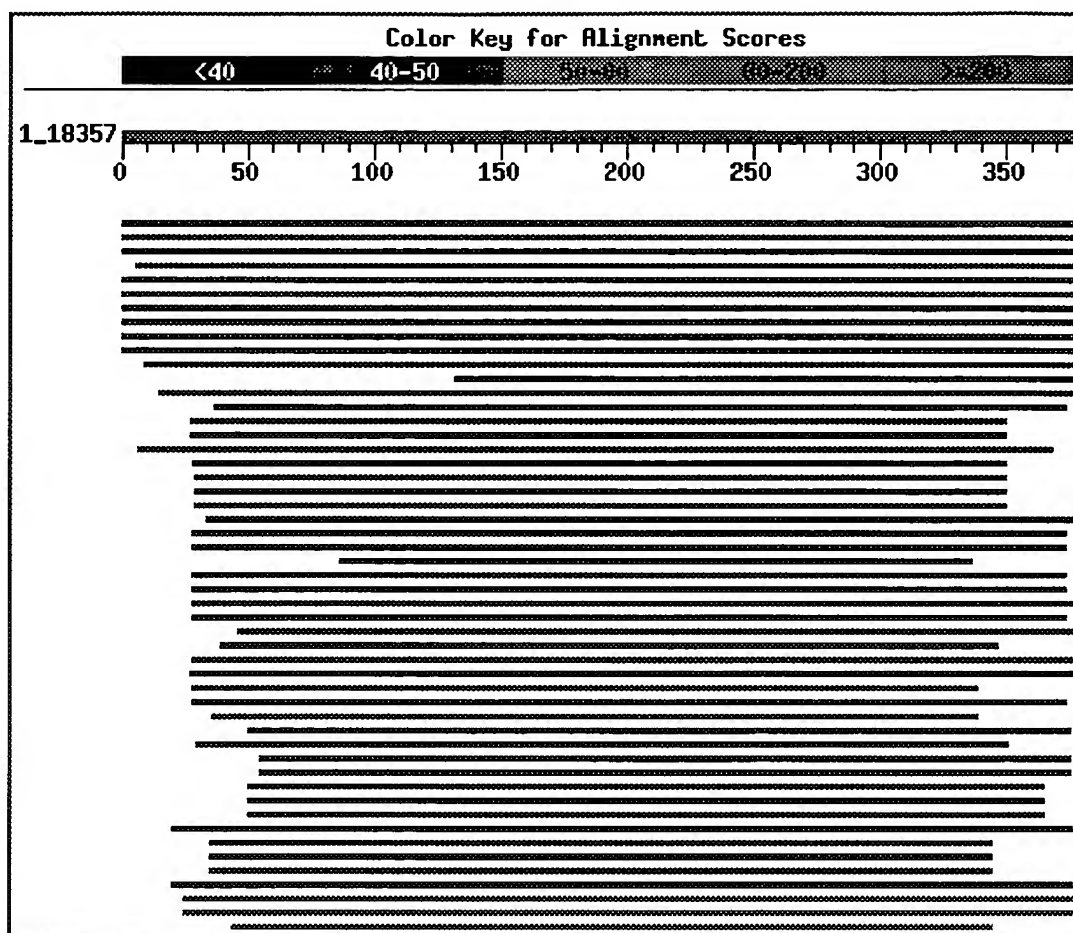
2,331,049 sequences; 790,373,496 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 501 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:			Score (bits)	E Value	
<u>gi 422826 pir A45680</u>	G protein-coupled peptide receptor EB...	<u>688</u>	0.0		
<u>gi 4502641 ref NP_001829.1 </u>	chemokine (C-C motif) receptor ...	<u>682</u>	0.0		
<u>gi 31127005 qb AAN47099.2 </u>	CC chemokine receptor 7 [Macaca ...	<u>675</u>	0.0		
<u>gi 55645367 ref XP_511477.1 </u>	PREDICTED: chemokine (C-C moti...	<u>669</u>	0.0		
<u>gi 56553516 qb AAV97930.1 </u>	chemokine receptor 7 [Bos taurus]	<u>635</u>	0.0		
<u>gi 48374059 ref NP_001001532.1 </u>	chemokine (C-C motif) recep...	<u>634</u>	e-180		
<u>gi 57091575 ref XP_548131.1 </u>	PREDICTED: similar to chemokin...	<u>625</u>	e-178		
<u>gi 26332358 db BAC29909.1 </u>	unnamed protein product [Mus mu...	<u>603</u>	e-171		
<u>gi 6671772 ref NP_031745.1 </u>	chemokine (C-C motif) receptor ...	<u>601</u>	e-171		
<u>gi 58477681 qb AAH89762.1 </u>	Chemokine (C-C motif) receptor 7...	<u>601</u>	e-170		
<u>gi 50760889 ref XP_425875.1 </u>	PREDICTED: similar to CC chemo...	<u>421</u>	e-116		
<u>gi 33415854 qb AAQ18436.1 </u>	chemokine receptor 7 [Bos taurus]	<u>409</u>	e-113		
<u>gi 49118818 qb AAH73273.1 </u>	MGC80638 protein [Xenopus laevis]	<u>375</u>	e-102		
<u>gi 47223975 emb CAG06152.1 </u>	unnamed protein product [Tetrao...	<u>286</u>	9e-76		
<u>gi 14043042 ref NP_112477.1 </u>	chemokine (C-C motif) receptor...	<u>251</u>	2e-65		
<u>gi 14043044 ref NP_006632.2 </u>	chemokine (C-C motif) receptor...	<u>251</u>	2e-65		
<u>gi 57101682 ref XP_541909.1 </u>	PREDICTED: similar to chemokin...	<u>250</u>	4e-65		
<u>gi 6753462 ref NP_034043.1 </u>	chemokine (C-C motif) receptor ...	<u>247</u>	3e-64		

gi 27229230 ref NP_758832.1	chemokine (C-C motif) receptor...	247	4e-64	G
gi 48675913 ref NP_001001624.1	chemokine C-C motif recepto...	245	1e-63	G
gi 41688290 dbj BAD08644.1	chemokine (C-C motif) receptor ...	245	1e-63	G
gi 34853814 ref XP_217862.2	similar to G protein-coupled r...	231	2e-59	G
gi 1668738 emb CAB02144.1	G PROTEIN-COUPLED RECEPTOR CKR-L...	229	1e-58	G
gi 37188165 ref NP_113597.2	chemokine (C-C motif) receptor...	229	1e-58	G
gi 47221187 emb CAG05508.1	unnamed protein product [Tetrao...	229	1e-58	
gi 55627742 ref XP_527565.1	PREDICTED: chemokine (C-C moti...	228	2e-58	G
gi 1870669 gb AAC51125.1	G protein-coupled receptor [Homo ...	228	2e-58	G
gi 24137229 gb AAN47098.1	CC chemokine receptor 6 [Macaca ...	228	3e-58	
gi 6753318 ref NP_033965.1	chemokine (C-C motif) receptor ...	228	3e-58	G
gi 2655885 emb CAA05917.1	chemokine receptor [Oncorhynchus...	227	5e-58	
gi 50741692 ref XP_419608.1	PREDICTED: similar to C-C chem...	226	8e-58	G
gi 5478218 dbj BAA82443.1	CC Chemokine LARC specific recep...	223	5e-57	G
gi 57032273 ref XP_541197.1	PREDICTED: hypothetical protei...	223	7e-57	G
gi 34740125 dbj BAC87714.1	C-C chemokine receptor 9 [Paral...	222	1e-56	
gi 1515435 gb AAB06949.1	IL8-related receptor [Homo sapiens]	221	2e-56	G
gi 47212478 emb CAF90274.1	unnamed protein product [Tetrao...	217	4e-55	
gi 48675917 ref NP_001001623.1	chemokine C-X-C motif recep...	214	2e-54	G
gi 52354647 gb AAH82897.1	LOC494782 protein [Xenopus laevis]	213	7e-54	G
gi 11342662 gb AAG34367.1	chemokine receptor CXCR6 [Mus mu...	213	9e-54	G
gi 13507658 ref NP_109637.1	chemokine (C-X-C motif) recept...	211	4e-53	G
gi 59857715 gb AAX08692.1	G protein-coupled receptor TYMST...	207	3e-52	
gi 59857629 gb AAX08649.1	G protein-coupled receptor TYMST...	205	2e-51	
gi 59858157 gb AAX08913.1	G protein-coupled receptor TYMST...	204	3e-51	
gi 30795217 ref NP_848540.1	chemokine (C-C motif) receptor...	204	4e-51	G
gi 15028430 gb AAK81712.1	chemokine receptor CCR11 [Mus mu...	203	6e-51	G
gi 26326635 dbj BAC27061.1	unnamed protein product [Mus mu...	202	1e-50	G
gi 21746187 ref NP_663746.1	chemokine (C-C motif) receptor...	202	1e-50	G
gi 55621142 ref XP_526311.1	PREDICTED: chemokine (C-C moti...	202	2e-50	G
gi 59857673 gb AAX08671.1	chemokine (C-C motif) receptor-l...	198	2e-49	
gi 27806269 ref NP_776690.1	chemokine (C-C motif) receptor...	197	3e-49	G
gi 42557662 emb CAF28781.1	C-C chemokine receptor 9 like [...	197	5e-49	
gi 50733072 ref XP_426014.1	PREDICTED: similar to C-C chem...	197	5e-49	G
gi 50978648 ref NP_001003020.1	CC chemokine receptor 4 [Ca...	196	9e-49	G
gi 2258402 gb AAB64225.1	Bonzo [Cercopithecus aethiops] >g...	194	3e-48	
gi 4877755 gb AAD31419.1	chemokine receptor bonzo [Macaca ...	194	3e-48	
gi 32481999 gb AAP84352.1	chemokine receptor 4 [Homo sapie...	194	4e-48	G
gi 50733078 ref XP_426017.1	PREDICTED: similar to CC chemo...	194	4e-48	G
gi 6467137 dbj BAA86966.1	b-chemokine receptor CCR4 [Homo ...	194	4e-48	G
gi 6467141 dbj BAA86968.1	b-chemokine receptor CCR4 [Homo ...	194	4e-48	G
gi 26449155 ref NP_598216.2	chemokine (C-C) receptor 4 [Ra...	193	6e-48	G
gi 13430093 gb AAK25742.1	orphan seven transmembrane recep...	193	6e-48	
gi 2258400 gb AAB64224.1	Bonzo [Macaca nemestrina] >gi 312...	193	8e-48	
gi 7716472 gb AAF68392.1	STRL33 [Cercopithecus torquatus atys]	192	1e-47	
gi 57113977 ref NP_001009051.1	chemokine (C-X-C motif) rec...	192	2e-47	G
gi 915274 gb AAA92582.1	chemokine receptor [Mus musculus]	191	3e-47	G
gi 32482007 gb AAP84356.1	chemokine receptor 6 [Homo sapie...	190	5e-47	G
gi 10716828 gb AAG21918.1	mutant G protein-coupled recepto...	190	5e-47	G

gi 50760178 ref XP_417922.1	PREDICTED: similar to putative...	190	6e-47	G
gi 6857773 ref NP_034046.1	chemokine (C-C motif) receptor ...	189	1e-46	G
gi 2209288 gb AAB61457.1	G protein-coupled receptor STRL33...	189	1e-46	G
gi 18034373 gb AAL57488.1	CC-chemokine receptor 4 [Cavia p...	187	4e-46	
gi 840784 emb CAA48723.1	MDCR15 protein [Homo sapiens] >gi...	187	4e-46	G
gi 56553518 gb AAV97931.1	chemokine receptor 3 [Bos taurus...	187	5e-46	G
gi 5514619 gb AAD44012.1	CC chemokine receptor type 5 [Cer...	187	5e-46	
gi 5713011 gb AAD47707.1	C-C chemokine receptor 5 [Macaca ...	186	7e-46	
gi 6753458 ref NP_034040.1	chemokine (C-X-C motif) recepto...	186	7e-46	G
gi 27753515 db BAC55184.1	CXC chemokine receptor 3 [Capra...	186	7e-46	
gi 5514617 gb AAD44010.1	CC chemokine receptor type 5 [Cer...	186	7e-46	
gi 5713013 gb AAD47709.1	C-C chemokine receptor 5 [Macaca ...	186	9e-46	
gi 5514623 gb AAD44016.1	CC chemokine receptor type 5 [Cer...	186	9e-46	
gi 5514622 gb AAD44015.1	CC chemokine receptor type 5 [Cer...	186	9e-46	
gi 3282810 gb AAC40163.1	chemokine receptor CXCR3 [Mus mus...	186	9e-46	G
gi 14589869 ref NP_116743.1	Burkitt lymphoma receptor 1 is...	186	1e-45	G
gi 4502415 ref NP_001707.1	Burkitt lymphoma receptor 1 iso...	186	1e-45	G
gi 5579304 gb AAD45497.1	CC chemokine receptor type 5 [Cer...	186	1e-45	
gi 5713106 gb AAD47802.1	C-C chemokine receptor 5 [Cercopi...	185	2e-45	
gi 5713039 gb AAD47735.1	C-C chemokine receptor 5 [Macaca ...	185	2e-45	
gi 33578093 gb AAQ22367.1	CC chemokine receptor 5 [Macaca ...	185	2e-45	
gi 4406111 gb AAD19862.1	C-C chemokine receptor type 5 [Ma...	185	2e-45	
gi 5713068 gb AAD47764.1	C-C chemokine receptor 5 [Varecia...	185	2e-45	
gi 12407353 gb AAG53465.1	CC chemokine receptor type 5 [Ce...	185	2e-45	
gi 57111007 ref XP_536065.1	PREDICTED: similar to interleu...	184	3e-45	G
gi 5713098 gb AAD47794.1	C-C chemokine receptor 5 [Cercopi...	184	3e-45	
gi 5713044 gb AAD47740.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713043 gb AAD47739.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713035 gb AAD47731.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713031 gb AAD47727.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713029 gb AAD47725.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713028 gb AAD47724.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5713017 gb AAD47713.1	C-C chemokine receptor 5 [Macaca ...	184	3e-45	
gi 5579302 gb AAD45495.1	CC chemokine receptor type 5 [Cer...	184	3e-45	
gi 5514618 gb AAD44011.1	CC chemokine receptor type 5 [Cer...	184	3e-45	
gi 4102994 gb AAD01639.1	G-protein coupled chemokine recep...	184	3e-45	
gi 13873087 gb AAK43369.1	C-C chemokine receptor 5 [Miopit...	184	3e-45	
gi 2088633 gb AAC34132.1	chemokine receptor CCR5 [Macaca m...	184	3e-45	
gi 5713016 gb AAD47712.1	C-C chemokine receptor 5 [Macaca ...	184	4e-45	
gi 4894982 gb AAD32685.1	CC chemokine receptor 5 [Papio cy...	184	4e-45	
gi 13873073 gb AAK43362.1	C-C chemokine receptor 5 [Erythr...	184	4e-45	
gi 42475950 ref NP_031577.2	Burkitt lymphoma receptor 1 [M...	184	5e-45	G
gi 5713110 gb AAD47806.1	C-C chemokine receptor 5 [Erythro...	184	5e-45	
gi 5713105 gb AAD47801.1	C-C chemokine receptor 5 [Cercopi...	184	5e-45	
gi 5713069 gb AAD47765.1	C-C chemokine receptor 5 [Lemur c...	184	5e-45	
gi 5713045 gb AAD47741.1	C-C chemokine receptor 5 [Macaca ...	184	5e-45	
gi 5713033 gb AAD47729.1	C-C chemokine receptor 5 [Macaca ...	184	5e-45	
gi 5579303 gb AAD45496.1	CC chemokine receptor type 5 [Cer...	184	5e-45	
gi 5514621 gb AAD44014.1	CC chemokine receptor type 5 [Cer...	184	5e-45	
gi 5514615 gb AAD44008.1	CC chemokine receptor type 5 [Cer...	184	5e-45	
gi 4426827 gb AAD20555.1	CC chemokine receptor 5 [Cercopit...	184	5e-45	
gi 2347108 gb AAC51795.1	CC chemokine receptor-5 [Cercopit...	184	5e-45	
gi 1002741 gb AAC50505.1	GPR9	183	6e-45	G
gi 4504099 ref NP_001495.1	chemokine (C-X-C motif) recepto...	183	6e-45	G
gi 5713112 gb AAD47808.1	C-C chemokine receptor 5 [Erythro...	183	6e-45	
gi 5713108 gb AAD47804.1	C-C chemokine receptor 5 [Erythro...	183	6e-45	

gi 5713100 gb AAD47796.1 	C-C chemokine receptor 5 [Cercopi...	183	6e-45	
gi 5713090 gb AAD47786.1 	C-C chemokine receptor 5 [Cercopi...	183	6e-45	
gi 5713081 gb AAD47777.1 	C-C chemokine receptor 5 [Cercopi...	183	6e-45	
gi 5713065 gb AAD47761.1 	C-C chemokine receptor 5 [Cercopi...	183	6e-45	
gi 31455576 gb AAP55851.1 	CXC chemokine receptor transcrip...	183	6e-45	G
gi 2305194 gb AAB65738.1 	CCR5 receptor [Pan troglodytes]	183	6e-45	G
gi 5514620 gb AAD44013.1 	CC chemokine receptor type 5 [Cer...	183	6e-45	
gi 3135302 gb AAC39833.1 	chemokine receptor CCR5 [Cercoc...	183	6e-45	
gi 5713099 gb AAD47795.1 	C-C chemokine receptor 5 [Cercopi...	183	8e-45	
gi 5713092 gb AAD47788.1 	C-C chemokine receptor 5 [Erythro...	183	8e-45	
gi 5713091 gb AAD47787.1 	C-C chemokine receptor 5 [Mandrill...	183	8e-45	
gi 5713070 gb AAD47766.1 	C-C chemokine receptor 5 [Lemur c...	183	8e-45	
gi 5713051 gb AAD47747.1 	C-C chemokine receptor 5 [Papio p...	183	8e-45	
gi 5713038 gb AAD47734.1 	C-C chemokine receptor 5 [Macaca ...	183	8e-45	
gi 5713022 gb AAD47718.1 	C-C chemokine receptor 5 [Macaca ...	183	8e-45	
gi 5713019 gb AAD47715.1 	C-C chemokine receptor 5 [Macaca ...	183	8e-45	
gi 14582847 gb AAK69684.1 	chemokine receptor CCR5 [Cercoc...	183	8e-45	
gi 2281710 emb CAB02143.1 	G PROTEIN-COUPLED RECEPTOR CKR-L...	183	8e-45	G
gi 3135298 gb AAC39831.1 	chemokine receptor CCR5 [Cercoc...	183	8e-45	
gi 433947 emb CAA50673.1 	muBLR1 [Mus musculus] >gi 631736 ...	182	1e-44	G
gi 5713084 gb AAD47780.1 	C-C chemokine receptor 5 [Cercopi...	182	1e-44	
gi 5713066 gb AAD47762.1 	C-C chemokine receptor 5 [Cercopi...	182	1e-44	
gi 3694849 gb AAC62472.1 	chemokine receptor CCR5 [Cercoc...	182	1e-44	
gi 50732852 ref XP_418795.1 	PREDICTED: similar to C-C chem...	182	1e-44	G
gi 4406105 gb AAD19859.1 	C-C chemokine receptor type 5 [Py...	182	1e-44	
gi 4406101 gb AAD19857.1 	C-C chemokine receptor type 5 [Py...	182	1e-44	
gi 4406097 gb AAD19855.1 	C-C chemokine receptor type 5 [Tr...	182	1e-44	
gi 4406095 gb AAD19854.1 	C-C chemokine receptor type 5 [Tr...	182	1e-44	
gi 4894984 gb AAD32686.1 	CC chemokine receptor 5 [Cercopit...	182	1e-44	
gi 13873077 gb AAK43364.1 	C-C chemokine receptor 5 [Colobu...	182	1e-44	
gi 57101678 ref XP_541907.1 	PREDICTED: similar to chemokin...	182	1e-44	G
gi 5713074 gb AAD47770.1 	C-C chemokine receptor 5 [Saguinu...	182	1e-44	
gi 5713053 gb AAD47749.1 	C-C chemokine receptor 5 [Papio p...	182	1e-44	
gi 4406107 gb AAD19860.1 	C-C chemokine receptor type 5 [Py...	182	1e-44	
gi 5514614 gb AAD44007.1 	CC chemokine receptor type 5 [Pan...	182	1e-44	
gi 13873097 gb AAK43374.1 	C-C chemokine receptor 5 [Therop...	182	1e-44	
gi 13873079 gb AAK43365.1 	C-C chemokine receptor 5 [Nasali...	182	1e-44	
gi 13873069 gb AAK43360.1 	C-C chemokine receptor 5 [Mandri...	182	1e-44	
gi 5713113 gb AAD47809.1 	C-C chemokine receptor 5 [Erythro...	182	2e-44	
gi 5713064 gb AAD47760.1 	C-C chemokine receptor 5 [Colobus...	182	2e-44	
gi 5713056 gb AAD47752.1 	C-C chemokine receptor 5 [Papio p...	182	2e-44	
gi 5713020 gb AAD47716.1 	C-C chemokine receptor 5 [Macaca ...	182	2e-44	
gi 5712951 gb AAD47647.1 	C-C chemokine receptor 5 [Hylobat...	182	2e-44	
gi 2896820 gb AAC03243.1 	chemokine receptor CCR5 [Rattus n...	182	2e-44	G
gi 4894980 gb AAD32684.1 	CC chemokine receptor 5 [Colobus ...	182	2e-44	
gi 4426832 gb AAD20560.1 	CC chemokine receptor 5 [Gorilla ...	182	2e-44	
gi 13873121 gb AAK43386.1 	C-C chemokine receptor 5 [Gorill...	182	2e-44	
gi 13873067 gb AAK43359.1 	C-C chemokine receptor 5 [Mandri...	182	2e-44	
gi 12407355 gb AAG53466.1 	CC chemokine receptor type 5 [Ce...	182	2e-44	
gi 56553514 gb AAV97929.1 	chemokine receptor 5 [Bos taurus...	181	2e-44	G
gi 5713104 gb AAD47800.1 	C-C chemokine receptor 5 [Cercopi...	181	2e-44	
gi 5713096 gb AAD47792.1 	C-C chemokine receptor 5 [Cercopi...	181	2e-44	
gi 5713082 gb AAD47778.1 	C-C chemokine receptor 5 [Cercopi...	181	2e-44	
gi 5713048 gb AAD47744.1 	C-C chemokine receptor 5 [Papio p...	181	2e-44	
gi 5713037 gb AAD47733.1 	C-C chemokine receptor 5 [Macaca ...	181	2e-44	
gi 5712964 gb AAD47660.1 	C-C chemokine receptor 5 [Pan tro...	181	2e-44	
gi 5712949 gb AAD47645.1 	C-C chemokine receptor 5 [Hylobat...	181	2e-44	

gi 4426824 gb AAD20552.1 	CC chemokine receptor 5 [Macaca a...	181	2e-44	
gi 4426823 gb AAD20551.1 	CC chemokine receptor 5 [Macaca n...	181	2e-44	
gi 2245620 gb AAB62557.1 	CC chemokine receptor-5 [Pan trog...	181	2e-44	G
gi 5713114 gb AAD47810.1 	C-C chemokine receptor 5 [Erythro...	181	3e-44	
gi 5713083 gb AAD47779.1 	C-C chemokine receptor 5 [Hylobat...	181	3e-44	
gi 5713073 gb AAD47769.1 	C-C chemokine receptor 5 [Varecia...	181	3e-44	
gi 5713071 gb AAD47767.1 	C-C chemokine receptor 5 [Lemur c...	181	3e-44	
gi 5713058 gb AAD47754.1 	C-C chemokine receptor 5 [Mandrill...	181	3e-44	
gi 5713009 gb AAD47705.1 	C-C chemokine receptor 5 [Cercopi...	181	3e-44	
gi 5712958 gb AAD47654.1 	C-C chemokine receptor 5 [Gorilla...	181	3e-44	
gi 5712955 gb AAD47651.1 	C-C chemokine receptor 5 [Gorilla...	181	3e-44	
gi 16758152 ref NP_445867.1 	chemokine (C-X-C motif) recept...	181	3e-44	G
gi 4406113 gb AAD19863.1 	C-C chemokine receptor type 5 [Hy...	181	3e-44	
gi 4406103 gb AAD19858.1 	C-C chemokine receptor type 5 [Po...	181	3e-44	
gi 13873113 gb AAK43382.1 	C-C chemokine receptor 5 [Hyloba...	181	3e-44	
gi 13873083 gb AAK43367.1 	C-C chemokine receptor 5 [Hyloba...	181	3e-44	
gi 9502106 gb AAF87982.1 	CC chemokine receptor 5 [Cercopit...	181	3e-44	
gi 5713093 gb AAD47789.1 	C-C chemokine receptor 5 [Erythro...	181	4e-44	
gi 5713085 gb AAD47781.1 	C-C chemokine receptor 5 [Cercopi...	181	4e-44	
gi 5713072 gb AAD47768.1 	C-C chemokine receptor 5 [Varecia...	181	4e-44	
gi 5713055 gb AAD47751.1 	C-C chemokine receptor 5 [Papio p...	181	4e-44	
gi 5713042 gb AAD47738.1 	C-C chemokine receptor 5 [Macaca ...]	181	4e-44	
gi 5713034 gb AAD47730.1 	C-C chemokine receptor 5 [Macaca ...]	181	4e-44	
gi 5514616 gb AAD44009.1 	CC chemokine receptor type 5 [Cer...	181	4e-44	
gi 13873081 gb AAK43366.1 	C-C chemokine receptor 5 [Trachy...	181	4e-44	
gi 9502104 gb AAF87981.1 	CC chemokine receptor 5 [Hylobate...	181	4e-44	
gi 4757938 ref NP_000639.1 	chemokine (C-C motif) receptor ...	180	5e-44	G
gi 57113969 ref NP_001009046.1 	chemokine (C-C motif) recep...	180	5e-44	G
gi 5713079 gb AAD47775.1 	C-C chemokine receptor 5 [Cercopi...	180	5e-44	
gi 5712968 gb AAD47664.1 	C-C chemokine receptor 5 [Pongo p...	180	5e-44	
gi 5712966 gb AAD47662.1 	C-C chemokine receptor 5 [Pan tro...	180	5e-44	G
gi 5712961 gb AAD47657.1 	C-C chemokine receptor 5 [Pan tro...	180	5e-44	
gi 5712960 gb AAD47656.1 	C-C chemokine receptor 5 [Pan tro...	180	5e-44	
gi 48675899 ref NP_001001618.1 	chemokine C-C motif recepto...	180	5e-44	G
gi 23193462 gb AAN14531.1 	chemokine receptor CCR5 [Saimiri...	180	5e-44	
gi 2305120 gb AAB65701.1 	CCR5 receptor [Homo sapiens]	180	5e-44	G
gi 4502633 ref NP_000638.1 	chemokine (C-C motif) receptor ...	180	7e-44	G
gi 5713002 gb AAD47698.1 	C-C chemokine receptor 5 [Callith...	180	7e-44	
gi 51592090 ref NP_446412.2 	chemokine (C-C) receptor 5 [Ra...	180	7e-44	G
gi 54038473 gb AAH84427.1 	CXCR2 protein [Xenopus laevis] >...	180	7e-44	G
gi 57898982 db BAD86855.1 	CXC chemokine receptor 3 [Canis...	180	7e-44	G
gi 3135296 gb AAC39830.1 	chemokine receptor CCR5 [Cercocob...	180	7e-44	
gi 47208340 emb CAF88488.1 	unnamed protein product [Tetrao...	180	7e-44	
gi 90075 pir JQ1231	interleukin-8 receptor - rabbit >gi 12...	179	9e-44	
gi 5713054 gb AAD47750.1 	C-C chemokine receptor 5 [Papio p...	179	9e-44	
gi 5712977 gb AAD47673.1 	C-C chemokine receptor 5 [Homo sa...	179	9e-44	G
gi 42540827 gb AAS19314.1 	CCR5 chemokine receptor [Homo sa...	179	9e-44	G
gi 3694853 gb AAC62474.1 	chemokine receptor CCR5 [Cercocob...	179	9e-44	
gi 2305132 gb AAB65707.1 	CCR5 receptor [Homo sapiens]	179	9e-44	G
gi 3135300 gb AAC39832.1 	chemokine receptor CCR5 [Cercocob...	179	9e-44	
gi 6753466 ref NP_034045.1 	chemokine (C-C motif) receptor ...	179	1e-43	G
gi 57086223 ref XP_546496.1 	PREDICTED: similar to Burkitt ...	179	1e-43	G
gi 5712982 gb AAD47678.1 	C-C chemokine receptor 5 [Homo sa...	179	1e-43	G
gi 5712969 gb AAD47665.1 	C-C chemokine receptor 5 [Pongo p...	179	1e-43	

gi 5712963 gb AAD47659.1 	C-C chemokine receptor 5 [Pan tro...	179	1e-43	
gi 3694851 gb AAC62473.1 	chemokine receptor CCR5 [Cercoc...	179	1e-43	
gi 631602 pir A53752	interleukin-8 receptor (clone 5B1a) -...	179	1e-43	
gi 29169293 gb AAO65971.1 	chemokine receptor 5 [Homo sapie...	179	1e-43	G
gi 16758000 ref NP_445755.1 	Burkitt lymphoma receptor 1 [R...	179	1e-43	G
gi 5713087 gb AAD47783.1 	C-C chemokine receptor 5 [Alouatt...	179	1e-43	
gi 5713008 gb AAD47704.1 	C-C chemokine receptor 5 [Cercopi...	179	1e-43	
gi 5713003 gb AAD47699.1 	C-C chemokine receptor 5 [Callith...	179	1e-43	
gi 5712981 gb AAD47677.1 	C-C chemokine receptor 5 [Homo sa...	179	1e-43	G
gi 5712976 gb AAD47672.1 	C-C chemokine receptor 5 [Homo sa...	179	1e-43	G
gi 5712974 gb AAD47670.1 	C-C chemokine receptor 5 [Homo sa...	179	1e-43	G
gi 42540823 gb AAS19312.1 	CCR5 chemokine receptor [Homo sa...	179	1e-43	G
gi 4337456 gb AAM18131.1 	chemokine receptor 5 [Homo sapiens]	179	1e-43	G
gi 2305190 gb AAB65736.1 	CCR5 receptor [Homo sapiens] >gi ...	179	1e-43	G
gi 2305180 gb AAB65731.1 	CCR5 receptor [Homo sapiens]	179	1e-43	G
gi 2305168 gb AAB65725.1 	CCR5 receptor [Homo sapiens]	179	1e-43	G
gi 2305156 gb AAB65719.1 	CCR5 receptor [Homo sapiens]	179	1e-43	G
gi 2305142 gb AAB65712.1 	CCR5 receptor [Homo sapiens]	179	1e-43	G
gi 2305128 gb AAB65705.1 	CCR5 receptor [Homo sapiens]	179	1e-43	G
gi 58760247 gb AAW82038.1 	CC chemokine receptor 5 variant ...	179	1e-43	
gi 4206191 gb AAD11572.1 	chemokine receptor [Macaca mulatt...	179	1e-43	
gi 4200299 emb CAA08838.1 	CCR5 chemokine receptor [Felis c...	179	1e-43	G
gi 1321935 emb CAA62563.1 	interleukin-8 receptor type B [P...	179	1e-43	
gi 5712980 gb AAD47676.1 	C-C chemokine receptor 5 [Homo sa...	178	2e-43	G
gi 2305200 gb AAB65741.1 	CCR5 receptor [Pan troglodytes]	178	2e-43	G
gi 2305196 gb AAB65739.1 	CCR5 receptor [Pan troglodytes]	178	2e-43	G
gi 58760249 gb AAW82039.1 	CC chemokine receptor 5 variant ...	178	2e-43	
gi 23305852 gb AAN17315.1 	interleukin 8 receptor B CXCR2 [...]	178	3e-43	
gi 27805835 ref NP_776726.1 	chemokine (C-X-C motif) recept...	178	3e-43	G
gi 4504683 ref NP_001548.1 	interleukin 8 receptor beta [Ho...	178	3e-43	G
gi 2305176 gb AAB65729.1 	CCR5 receptor [Homo sapiens]	178	3e-43	G
gi 2305136 gb AAB65709.1 	CCR5 receptor [Homo sapiens]	178	3e-43	G
gi 57163789 ref NP_001009248.1 	chemokine receptor 5 [Felis...	177	3e-43	G
gi 5713005 gb AAD47701.1 	C-C chemokine receptor 5 [Alouatt...	177	3e-43	
gi 5712975 gb AAD47671.1 	C-C chemokine receptor 5 [Homo sa...	177	3e-43	G
gi 2305178 gb AAB65730.1 	CCR5 receptor [Homo sapiens]	177	3e-43	G
gi 13873089 gb AAK43370.1 	C-C chemokine receptor 5 [Callic...	177	3e-43	
gi 13873075 gb AAK43363.1 	C-C chemokine receptor 5 [Alouat...	177	3e-43	
gi 5713080 gb AAD47776.1 	C-C chemokine receptor 5 [Callith...	177	4e-43	
gi 23193460 gb AAN14530.1 	chemokine receptor CCR5 [Callith...	177	4e-43	
gi 33521604 gb AAQ20014.1 	CC chemokine receptor 5 [Callith...	177	4e-43	
gi 2305158 gb AAB65720.1 	CCR5 receptor [Homo sapiens]	177	4e-43	G
gi 1935045 gb AAB51765.1 	fusin [Felis catus]	177	4e-43	G
gi 9502108 gb AAF87983.1 	CC chemokine receptor 5 [Lagothri...	177	4e-43	
gi 5712948 gb AAD47644.1 	C-C chemokine receptor 5 [Hylobat...	177	6e-43	
gi 33521602 gb AAQ20013.1 	CC chemokine receptor 5 [Callith...	177	6e-43	
gi 2305148 gb AAB65715.1 	CCR5 receptor [Homo sapiens]	177	6e-43	G
gi 13873085 gb AAK43368.1 	C-C chemokine receptor 5 [Ateles...	177	6e-43	
gi 2347114 gb AAC53386.1 	CC chemokine receptor-5 [Mus musc...	177	6e-43	G
gi 1237134 gb AAC52453.1 	JE receptor	176	7e-43	G

gi 57100809 ref XP_541020.1 	PREDICTED: hypothetical protei...	176	7e-43	G
gi 2896818 gb AAC03242.1 	chemokine receptor CCR2 [Rattus n...	176	7e-43	G
gi 58760245 gb AAW82037.1 	CC chemokine receptor 5 variant ...	176	1e-42	
gi 58652135 ref NP_001011675.1 	Burkitt lymphoma receptor 1...	176	1e-42	G
gi 6002764 gb AAF00130.1 	chemokine receptor CXCR4-Lo [Homo...	176	1e-42	G
gi 33521612 gb AAQ20018.1 	CC chemokine receptor 5 [Leontop...	176	1e-42	
gi 33521606 gb AAQ20015.1 	CC chemokine receptor 5 [Leontop...	176	1e-42	
gi 2305124 gb AAB65703.1 	CCR5 receptor [Homo sapiens]	176	1e-42	G
gi 60097918 ref NP_001012342.2 	chemokine (C-C motif) recep...	176	1e-42	
gi 1842247 gb AAC48852.1 	CXCR-4 homolog [Felis catus] >gi ...	176	1e-42	G
gi 3059120 emb CAA12166.1 	CXCR4 [Homo sapiens]	176	1e-42	G
gi 2305140 gb AAB65711.1 	CCR5 receptor [Homo sapiens]	175	2e-42	G
gi 3243095 gb AAC23950.1 	putative chemokine receptor [Gall...	175	2e-42	
gi 9502112 gb AAF87985.1 	CC chemokine receptor 5 [Ateles sp.]	175	2e-42	
gi 5713007 gb AAD47703.1 	C-C chemokine receptor 5 [Aotus t...	175	2e-42	
gi 47523298 ref NP_998938.1 	chemokine (C-X-C motif) recept...	175	2e-42	G
gi 23305854 gb AAN17316.1 	interleukin 8 receptor B CXCR2 [...]	175	2e-42	
gi 33521616 gb AAQ20020.1 	CC chemokine receptor 5 [Brachyt...	175	2e-42	
gi 2431976 gb AAB71183.1 	CCR5 [Mus musculus]	175	2e-42	G
gi 57113965 ref NP_001009047.1 	chemokine (C-X-C motif) rec...	174	3e-42	G
gi 42540825 gb AAS19313.1 	CCR5 chemokine receptor [Homo sa...	174	3e-42	G
gi 30584919 gb AAP36716.1 	Homo sapiens chemokine (C-X-C mo...	174	3e-42	
gi 33521610 gb AAQ20017.1 	CC chemokine receptor 5 [Leontop...	174	3e-42	
gi 49118568 gb AAH73571.1 	LOC443669 protein [Xenopus laevis]	174	3e-42	G
gi 2305166 gb AAB65724.1 	CCR5 receptor [Homo sapiens]	174	3e-42	G
gi 4100052 gb AAD00729.1 	CCR5 [Felis catus]	174	3e-42	G
gi 1698716 gb AAB37273.1 	beta chemokine receptor [Mus musc...	174	3e-42	G
gi 1321889 emb CAA62565.1 	interleukin-8 receptor type B [M...	174	3e-42	
gi 9587720 gb AAF89352.1 	chemokine receptor CXCR4 [Gorilla...	174	3e-42	
gi 9587716 gb AAF89350.1 	chemokine receptor CXCR4 [Hylobat...	174	3e-42	
gi 13549090 gb AAK29630.1 	chemokine receptor CXCR4 [Homo s...	174	4e-42	G
gi 9587714 gb AAF89349.1 	chemokine receptor CXCR4 [Hylobat...	174	4e-42	
gi 57111005 ref XP_536064.1 	PREDICTED: similar to interleu...	174	5e-42	G
gi 5712979 gb AAD47675.1 	C-C chemokine receptor 5 [Homo sa...	174	5e-42	G
gi 33521614 gb AAQ20019.1 	CC chemokine receptor 5 [Leontop...	174	5e-42	
gi 1321816 emb CAA62564.1 	interleukin-8 receptor type B [G...	174	5e-42	
gi 9587724 gb AAF89354.1 	chemokine receptor CXCR4 [Ateles ...]	174	5e-42	
gi 35187401 gb AAQ84305.1 	CXC chemokine receptor 1-like pr...	173	6e-42	G
gi 5712985 gb AAD47681.1 	C-C chemokine receptor 5 [Saguinu...	173	6e-42	
gi 31044501 gb AAQ47588.2 	chemokine receptor CXCR4 [Tupaia...	173	6e-42	
gi 2305192 gb AAB65737.1 	CCR5 receptor [Homo sapiens]	173	6e-42	G
gi 5712992 gb AAD47688.1 	C-C chemokine receptor 5 [Saguinu...	173	8e-42	
gi 33521608 gb AAQ20016.1 	CC chemokine receptor 5 [Leontop...	173	8e-42	
gi 57157736 db BAD83840.1 	CC chemokine receptor 5 [Canis ...]	173	8e-42	G
gi 9587722 gb AAF89353.1 	chemokine receptor CXCR4 [Alouatt...	173	8e-42	
gi 2851566 sp P51682 CKR5 MOUSE	C-C chemokine receptor type...	173	8e-42	G
gi 57101676 ref XP_541906.1 	PREDICTED: similar to chemokin...	172	1e-41	G
gi 5712990 gb AAD47686.1 	C-C chemokine receptor 5 [Saguinu...	172	1e-41	
gi 5712983 gb AAD47679.1 	C-C chemokine receptor 5 [Saguinu...	172	1e-41	
gi 23193458 gb AAN14529.1 	chemokine receptor CXCR4 [Saimir...	172	1e-41	
gi 9587732 gb AAF89358.1 	chemokine receptor CXCR4 [Pitheci...	172	1e-41	
gi 31542356 ref NP_034047.2 	chemokine (C-C motif) receptor...	172	1e-41	G

gi 23193456 gb AAN14528.1 	chemokine receptor CXCR4 [Callit...	172	1e-41	
gi 13430095 gb AAK25743.1 	chemokine receptor CXCR4 [Macaca...	172	1e-41	
gi 2625094 gb AAC63631.1 	CXC chemokine receptor 4 [Papio c...	172	1e-41	
gi 4467415 emb CAB37671.1 	interleukin-8 receptor type A [G...	172	1e-41	
gi 9587730 gb AAF89357.1 	chemokine receptor CXCR4 [Callice...	172	1e-41	
gi 9587696 gb AAF89340.1 	chemokine receptor CXCR4 [Presbyt...	172	1e-41	
gi 42557658 emb CAF28777.1 	C-C chemokine receptor 5 like [...]	172	2e-41	
gi 6318165 emb CAB60252.1 	CXC chemokine receptor 4 [Acipen...	172	2e-41	
gi 8393600 ref NP_058879.1 	interleukin 8 receptor, beta [R...	172	2e-41	G
gi 50732854 ref XP_418796.1 	PREDICTED: similar to C-C chem...	171	2e-41	G
gi 17902281 gb AAL47855.1 	chemokine receptor CXCR4 [Rattus...	171	2e-41	G
gi 1419629 emb CAA63867.1 	MIP-1 alpha receptor [Mus musculus]	171	2e-41	G
gi 3294342 db BAA31327.1 	CXCR4 receptor [Cercopithecus ae...	171	2e-41	
gi 9587698 gb AAF89341.1 	chemokine receptor CXCR4 [Mandrill...	171	2e-41	
gi 9587690 gb AAF89337.1 	chemokine receptor CXCR4 [Presbyt...	171	2e-41	
gi 5713006 gb AAD47702.1 	C-C chemokine receptor 5 [Aotus t...	171	3e-41	
gi 5712988 gb AAD47684.1 	C-C chemokine receptor 5 [Saguinu...	171	3e-41	
gi 48675907 ref NP_001001619.1 	chemokine C-C motif recepto...	171	3e-41	G
gi 4102992 gb AAD01638.1 	G-protein coupled receptor; CXCR4...	171	3e-41	
gi 2911294 gb AAC39641.1 	alpha-chemokine receptor 4 [Macac...	171	3e-41	
gi 1906613 gb AAB50408.1 	CXC chemokine receptor [Rattus no...	171	3e-41	G
gi 9587708 gb AAF89346.1 	chemokine receptor CXCR4 [Macaca ...]	171	3e-41	
gi 9587700 gb AAF89342.1 	chemokine receptor CXCR4 [Mandrill...	171	3e-41	
gi 298783 gb AAB25879.1 	interleukin-8 receptor type 1, IL8...	171	4e-41	G
gi 5712989 gb AAD47685.1 	C-C chemokine receptor 5 [Saguinu...	171	4e-41	
gi 7230482 gb AAF42991.1 	CXC chemokine receptor 4 [Hylobat...	171	4e-41	
gi 9587688 gb AAF89336.1 	chemokine receptor CXCR4 [Presbyt...	171	4e-41	
gi 5712993 gb AAD47689.1 	C-C chemokine receptor 5 [Saguinu...	170	5e-41	
gi 1899056 gb AAC51159.1 	CXCR4 gene product [Macaca mulatt...	170	5e-41	
gi 9587728 gb AAF89356.1 	chemokine receptor CXCR4 [Callimi...	170	5e-41	
gi 57163985 ref NP_001009241.1 	chemokine (C-C motif) recep...	170	7e-41	G
gi 9506809 ref NP_062183.1 	interleukin 8 receptor, alpha [...]	170	7e-41	G
gi 27805943 ref NP_776785.1 	interleukin 8 receptor, beta [...]	170	7e-41	G
gi 23305862 gb AAN17320.1 	interleukin 8 receptor B CXCR2 [...]	170	7e-41	
gi 7141318 gb AAF37288.1 	CXCR4 receptor [Saimiri boliviensis]	170	7e-41	
gi 9587726 gb AAF89355.1 	chemokine receptor CXCR4 [Callith...	170	7e-41	
gi 4502631 ref NP_001286.1 	chemokine (C-C motif) receptor ...	169	9e-41	G
gi 5712994 gb AAD47690.1 	C-C chemokine receptor 5 [Saguinu...	169	9e-41	
gi 23305858 gb AAN17318.1 	interleukin 8 receptor B CXCR2 [...]	169	9e-41	
gi 219863 db BAA01723.1 	HM145 [Homo sapiens]	169	9e-41	G
gi 7441609 pir G00048	fusin (LESTRA) - crab-eating macaque...	169	9e-41	
gi 9587738 gb AAF89361.1 	chemokine receptor CXCR4 [Nyctice...	169	9e-41	
gi 1237136 gb AAC52454.1 	MIP-1 alpha receptor	169	1e-40	G
gi 4504681 ref NP_000625.1 	interleukin 8 receptor alpha [H...	169	1e-40	G
gi 27802639 gb AAO21209.1 	chemokine receptor CXCR4 [Petrom...	169	1e-40	
gi 20380431 gb AAH28221.1 	Interleukin 8 receptor alpha [Ho...	169	1e-40	G
gi 1934671 gb AAB54116.1 	alpha chemokine receptor [Macaca ...]	169	1e-40	
gi 4467981 emb CAB37850.1 	interleukin-8 receptor type A [P...	169	1e-40	
gi 55741694 ref NP_001003151.1 	interleukin-8 receptor [Can...	169	2e-40	G
gi 10120494 ref NP_065417.1 	macrophage inflammatory protei...	169	2e-40	G
gi 45382915 ref NP_989948.1 	chemokine receptor CXCR4 [Gall...	169	2e-40	G
gi 3135304 gb AAC39834.1 	chemokine receptor CXCR4 [Cercoc...	169	2e-40	
gi 7108519 gb AAF36453.1 	chemokine receptor [Callithrix ja...	169	2e-40	
gi 48675909 ref NP_001001621.1 	chemokine C-C motif recepto...	168	2e-40	G

gi 11024708 ref NP_031747.2	G protein-coupled receptor 2 [...	168	3e-40	G
gi 48735085 gb AAH72397.1	Interleukin 8 receptor alpha [Ho...	168	3e-40	G
gi 34873846 ref XP_343969.1	similar to 7-transmembrane G-p...	167	3e-40	G
gi 55616095 ref XP_526027.1	PREDICTED: similar to High aff...	167	3e-40	G
gi 23305856 gb AAN17317.1	interleukin 8 receptor B CXCR2 [...	167	3e-40	
gi 2305126 gb AAB65704.1	CCR5 receptor [Homo sapiens]	167	3e-40	G
gi 7230484 gb AAF42992.1	CXC chemokine receptor 4 [Saguinu...	167	3e-40	
gi 7230480 gb AAF42990.1	CXC chemokine receptor 4 [Cercopi...	167	3e-40	
gi 9587740 gb AAF89362.1	chemokine receptor CXCR4 [Eulemur...	167	3e-40	
gi 7108517 gb AAF36452.1	chemokine receptor [Oryctolagus c...	167	4e-40	
gi 6753456 ref NP_034039.1	interleukin 8 receptor beta [Mu...	167	6e-40	G
gi 6753460 ref NP_034041.1	chemokine (C-X-C motif) recepto...	167	6e-40	G
gi 29602789 gb AAO84922.1	interleukin-8 receptor CXCR2 [Ca...	167	6e-40	
gi 17223091 gb AAL18011.1	Cxcr4A [Danio rerio]	167	6e-40	G
gi 7546849 gb AAF63711.1	CC chemokine receptor 10B [Mus mu...	167	6e-40	G
gi 7546847 gb AAF63710.1	CC chemokine receptor 10A [Mus mu...	167	6e-40	G
gi 1542889 emb CAB02202.1	CXCR-4 [Mus musculus]	167	6e-40	G
gi 543400 pir S42096	interleukin-8 receptor - rat	167	6e-40	
gi 1666649 emb CAA67894.1	leukocyte-derived seven transmem...	166	8e-40	G
gi 9587742 gb AAF89363.1	chemokine receptor CXCR4 [Perodic...	166	8e-40	
gi 57091477 ref XP_548084.1	PREDICTED: similar to hypothet...	166	1e-39	G
gi 39016879 gb AAR07898.1	CC chemokine receptor 10 [Homo s...	165	2e-39	G
gi 23305860 gb AAN17319.1	interleukin 8 receptor B CXCR2 [...	165	2e-39	
gi 47215024 emb CAG01848.1	unnamed protein product [Tetrao...	165	2e-39	
gi 34223272 gb AAO66450.1	CXCR4 [Macaca fascicularis] >gi ...	163	6e-39	
gi 40254673 ref NP_571957.2	chemokine (C-X-C motif) recept...	163	6e-39	G
gi 5712991 gb AAD47687.1	C-C chemokine receptor 5 [Saguinu...	163	8e-39	
gi 55250561 gb AAH85659.1	Zgc:92301 [Danio rerio] >gi 5592...	162	1e-38	G
gi 52546730 ref NP_001005261.1	C-C chemokine receptor 3 [C...	162	1e-38	G
gi 55620263 ref XP_526193.1	PREDICTED: CC chemokine recept...	162	1e-38	G
gi 50732904 ref XP_418820.1	PREDICTED: similar to CX3C che...	162	1e-38	G
gi 47218519 emb CAF98051.1	unnamed protein product [Tetrao...	162	1e-38	
gi 9628081 ref NP_042675.1	G protein-coupled receptor [Equ...	162	2e-38	G
gi 37655185 gb AAO65970.2	chemokine receptor 3 [Homo sapie...	162	2e-38	G
gi 42557657 emb CAF28776.1	C-C chemokine receptor 11 like ...	162	2e-38	
gi 2137554 pir I49341	MIP-1 alpha receptor like-2 - mouse	161	2e-38	
gi 7705316 ref NP_057686.1	CC chemokine receptor 10 [Homo ...	161	2e-38	G
gi 52138984 gb AAH82709.1	LOC494705 protein [Xenopus laevis]	161	2e-38	G
gi 1203601 gb AAA89155.1	MIP-1 alpha receptor like-2	161	2e-38	G
gi 3551197 dbj BAA32797.1	CXCR4 [Cyprinus carpio]	161	2e-38	
gi 577415 gb AAA64593.1	G protein-coupled receptor	161	3e-38	G
gi 1109784 gb AAA86118.1	chemokine G-protein-coupled recep...	161	3e-38	G
gi 48675903 ref NP_001001620.1	chemokine C-C motif recepto...	161	3e-38	G
gi 57157738 dbj BAD83841.1	CC chemokine receptor 3 [Canis ...	160	4e-38	G
gi 1477561 gb AAR09726.1	C-C chemokine receptor 3 >gi 7441...	160	4e-38	G
gi 1082383 pir B55733	G protein-coupled receptor GPR2 - hu...	160	5e-38	
gi 22074362 gb AAL13085.1	eotaxin receptor [Mus musculus] ...	159	9e-38	G
gi 15029747 gb AAH11092.1	Chemokine (C-C motif) receptor 1...	159	9e-38	G
gi 27721857 ref XP_236742.1	similar to MIP-1 alpha recepto...	159	9e-38	G

gi 27924174 gb AAH44963.1 	Cxcr4-prov protein [Xenopus laevis]	159	1e-37	G
gi 31542352 ref NP_034042.2 	chemokine (C-C motif) receptor...	159	1e-37	G
gi 49115863 gb AAH73603.1 	Unknown (protein for MGC:82907) ...	159	1e-37	
gi 8118035 gb AAF72871.1 	7-transmembrane G-protein coupled...	159	1e-37	G
gi 3327018 emb CAA04493.1 	CXC chemokine receptor [Oncorhyn...	159	2e-37	
gi 47220226 emb CAF98991.1 	unnamed protein product [Tetrao...	159	2e-37	
gi 26327025 dbj BAC27256.1 	unnamed protein product [Mus mu...	159	2e-37	G
gi 881548 gb AAA89153.1 	macrophage inflammatory protein-1 ...	158	2e-37	G
gi 1109786 gb AAA86119.1 	chemokine G-protein-coupled recep...	158	2e-37	G
gi 2407217 gb AAB70526.1 	chemokine receptor [Macaca mulatt...	158	2e-37	
gi 31542354 ref NP_034044.2 	CC chemokine receptor 3 [Mus m...	157	4e-37	G
gi 50732143 ref XP_418499.1 	PREDICTED: similar to CC-chemo...	157	5e-37	G
gi 6467133 dbj BAA86964.1 	b-chemokine receptor CCR3 [Homo ...	157	6e-37	G
gi 16758844 ref NP_446410.1 	CC chemokine receptor 3 [Rattu...	156	8e-37	G
gi 50540418 ref NP_001002675.1 	zgc:91924 [Danio rerio] >gi...	156	1e-36	G
gi 18858507 ref NP_571909.1 	chemokine (C-X-C motif), recep...	156	1e-36	G
gi 3930519 gb AAC80428.1 	C-C chemokine receptor 3 [Cavia p...	156	1e-36	
gi 2897073 gb AAC03337.1 	chemokine receptor CCR3 [Rattus n...	155	2e-36	G
gi 13929467 ref NP_001287.2 	chemokine binding protein 2 [H...	154	4e-36	G
gi 30583827 gb AAP36162.1 	Homo sapiens chemokine binding p...	154	4e-36	
gi 30171328 gb AAP20651.1 	chemokine-binding protein 2 [Hom...	154	4e-36	G
gi 2213809 gb AAB97728.1 	CC-chemokine-binding receptor JAB...	154	5e-36	G
gi 51870077 ref YP_073630.1 	Hypothetical protein LDVICp124...	153	7e-36	G
gi 2266686 emb CAA74107.1 	C-C chemokine receptor-3 [Macaca...	153	7e-36	
gi 2266434 emb CAA74106.1 	C-C chemokine receptor-3 [Cercop...	153	9e-36	
gi 4885121 ref NP_005192.1 	chemokine (C-C motif) receptor ...	152	1e-35	G
gi 55620239 ref XP_526178.1 	PREDICTED: chemokine (C-C moti...	152	1e-35	G
gi 30962608 gb AAP42156.1 	chemokine receptor D6 [Homo sapi...	152	1e-35	G
gi 42557659 emb CAF28778.1 	C-C chemokine receptor 8 like [...	152	1e-35	
gi 22652109 gb AAN03618.1 	eotaxin receptor CCR3 [Macaca mu...	152	1e-35	
gi 22652103 gb AAN03615.1 	eotaxin receptor CCR3 [Macaca fa...	152	1e-35	
gi 18071641 gb AAL55443.1 	chemokine receptor 3 [Macaca fas...	152	1e-35	
gi 18071639 gb AAL55442.1 	chemokine receptor 3 [Macaca fas...	152	1e-35	
gi 13027670 gb AAK08628.1 	CC chemokine receptor 8 [Homo sa...	152	1e-35	G
gi 2407219 gb AAB70527.1 	chemokine receptor [Macaca mulatt...	152	2e-35	
gi 6671770 ref NP_031744.1 	chemokine (C-C motif) receptor ...	151	3e-35	G
gi 57103782 ref XP_542719.1 	PREDICTED: similar to chemokin...	150	4e-35	G
gi 47220980 emb CAF98209.1 	unnamed protein product [Tetrao...	150	4e-35	
gi 3298340 dbj BAA31458.1 	CXC chemokine receptor-1 [Cyprin...	150	4e-35	
gi 347190 gb AAC37873.1 	G protein-coupled receptor >gi 586...	150	6e-35	
gi 18448639 gb AAL69885.1 	SPV146 G protein-coupled CC chem...	150	6e-35	G
gi 13430087 gb AAK25739.1 	chemokine receptor CCR3 [Macaca ...	150	6e-35	
gi 34740123 dbj BAC87713.1 	C-C chemokine receptor-3 [Paral...	149	2e-34	
gi 31542483 ref NP_067622.2 	D6 beta-chemokine receptor [Mu...	147	4e-34	G
gi 3851699 gb AAC72403.1 	chemokine receptor [Macaca mulatt...	147	4e-34	
gi 55562725 gb AAH86449.1 	Chemokine binding protein 2 [Rat...	147	6e-34	G
gi 57103810 ref XP_542737.1 	PREDICTED: similar to chemokin...	146	8e-34	G
gi 13897910 gb AAK48497.1 	IL-8 receptor [Oncorhynchus mykiss]	145	2e-33	
gi 13897920 gb AAK48502.1 	IL-8 receptor [Oncorhynchus mykiss]	145	2e-33	
gi 2213807 gb AAB61572.1 	CC-chemokine-binding receptor JAB...	145	2e-33	G

gi 2072651 emb CAA73379.1 	beta-chemokine receptor D6 [Mus ...	144	3e-33	G
gi 47227892 emb CAG09055.1 	unnamed protein product [Tetrao...	144	5e-33	
gi 109222 pir A23669	interleukin-8 receptor, high affinity...	143	7e-33	
gi 27721715 ref XP_236704.1 	similar to chemokine receptor ...	142	1e-32	G
gi 54038607 gb AAH84447.1 	Hypothetical LOC496477 [Xenopus ...	142	2e-32	G
gi 1354505 gb AAB01981.1 	chemokine receptor LCR1 [Rattus n...	141	3e-32	G
gi 3298358 dbj BAA31470.1 	CXC chemokine receptor-2 [Cyprin...	141	3e-32	
gi 19424190 ref NP_598218.1 	Rbs11 protein [Rattus norvegic...	140	5e-32	G
gi 13897918 gb AAK48501.1 	IL-8 receptor [Oncorhynchus myki...	140	5e-32	
gi 15215068 gb AAH12653.1 	Chemokine (C-X3-C) receptor 1 [M...	140	8e-32	G
gi 26331012 dbj BAC29236.1 	unnamed protein product [Mus mu...	140	8e-32	G

Alignments

Get selected sequences

Select all

Deselect all

☒ >[gi|422826|pir||A45680](#) G protein-coupled peptide receptor EBI 1 - human
[gi|183485|gb|AAA58615.1|](#) **G** EBV induced G-protein coupled receptor
 Length = 378

Score = 688 bits (1775), Expect = 0.0

Identities = 351/378 (92%), Positives = 351/378 (92%)

Query: 1 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
 Sbjct: 1 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60

Query: 61 LPIMYSIICFXXXXXXXXXXXXTYIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAK 120
 LPIMYSIICF TYIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAK 120
 Sbjct: 61 LPIMYSIICFVGLLGNGLVVLTYIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAK 120

Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180
 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180
 Sbjct: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180

Query: 181 GSAILATVLSIPELLYSDLQRSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMS 240
 GSAILATVLSIPELLYSDLQRSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMS 240
 Sbjct: 181 GSAILATVLSIPELLYSDLQRSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMS 240

Query: 241 FCYLVIIIRTLLQARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCEL 300
 FCYLVIIIRTLLQARNFERN QLPYNGVVLAQTVANFNITSSTCEL 300
 Sbjct: 241 FCYLVIIIRTLLQARNFERNKAIKVIIAVVVVFVIFQLPYNGVVLAQTVANFNITSSTCEL 300

Query: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 Sbjct: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360

Query: 361 IRRSSMSVEAETTTTFSP 378
 IRRSSMSVEAETTTTFSP
 Sbjct: 361 IRRSSMSVEAETTTTFSP 378

>gi|4502641|ref|NF_001829.1| **G** chemokine (C-C motif) receptor 7 precursor [Homo
 gi|23243434|gb|AAH35343.1| **G** Chemokine (C-C motif) receptor 7, precursor [Homo sa
 gi|49176610|gb|AAT52232.1| **G** CC chemokine receptor 7 [Homo sapiens]
 gi|468316|gb|AAA74230.1| **G** G protein-coupled receptor [Homo sapiens]
 gi|1082381|pir|B55735 lymphocyte-specific G protein-coupled receptor EBI1 - huma
 gi|468320|gb|AAA74231.1| **G** G protein-coupled receptor
 gi|1352335|sp|P32248|CKR7_HUMAN **G** C-C chemokine receptor type 7 precursor (C-C CK
 (CCR-7) (MIP-3 beta receptor) (EBV-induced G
 protein-coupled receptor 1) (EBI1) (BLR2)
 Length = 378

Score = 682 bits (1760), Expect = 0.0

Identities = 348/378 (92%), Positives = 349/378 (92%)

Query: 1 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF
 Sbjct: 1 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60

Query: 61 LPIMYSIICFXXXXXXXXXXXXTYIYFKRLKTMDDTYLLNLAVADILFLLTLPFWAYSAAK 120
 LPIMYSIICF TYIYFKRLKTMDDTYLLNLAVADILFLLTLPFWAYSAAK
 Sbjct: 61 LPIMYSIICFVGLLGNGLVVLTYIYFKRLKTMDDTYLLNLAVADILFLLTLPFWAYSAAK 120

Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180
 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV
 Sbjct: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180

Query: 181 GSAILATVLSIPELLYSDLQRSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMS 240
 G ILATVLSIPELLYSDLQRSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMS
 Sbjct: 181 GIWILATVLSIPELLYSDLQRSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMS 240

Query: 241 FCYLVIIIRTLLQARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCEL 300
 FCYLVIIIRTLLQARNFERN QLPYNGVVLAQTVANFNITSSTCEL
 Sbjct: 241 FCYLVIIIRTLLQARNFERNKAIKVIIAVVVVIFVQLPYNGVVLAQTVANFNITSSTCEL 300

Query: 301 SKQLNIAVDVITYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 SKQLNIAVDVITYSLACVRCCVNPFLYAFIGVKFRND+FKLFKDLGCLSQEQLRQWSSCRH
 Sbjct: 301 SKQLNIAVDVITYSLACVRCCVNPFLYAFIGVKFRNDLFLFKDLGCLSQEQLRQWSSCRH 360

Query: 361 IRRSSMSVEAETTTTFSP 378
 IRRSSMSVEAETTTTFSP
 Sbjct: 361 IRRSSMSVEAETTTTFSP 378

>gi|31127005|gb|AAN47099.2| CC chemokine receptor 7 [Macaca mulatta]
 Length = 378

Score = 675 bits (1742), Expect = 0.0

Identities = 346/378 (91%), Positives = 347/378 (91%)

Query: 1 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
 MDLGKPMKSVLVVALLVIFQV LCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF
 Sbjct: 1 MDLGKPMKSVLVVALLVIFQVYLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60

Query: 61 LPIMYSIICFXXXXXXXXXXXXTYIYFKRLKTMDDTYLLNLAVADILFLLTLPFWAYSAAK 120
 LPIMYSIICF . TYIYFKRLKTMDDTYLLNLAVADILFLLTLPFWAYSAAK
 Sbjct: 61 LPIMYSIICFVGLLGNGLVVLTYIYFKRLKTMDDTYLLNLAVADILFLLTLPFWAYSAAK 120



Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180
 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV
 Sbjct: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180

Query: 181 GSAILATVLSIPELLYSGLQSSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMS 240
 G ILATVLSIPELLYS LQSSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMS
 Sbjct: 181 GIWILATVLSIPELLYSGLQSSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMS 240

Query: 241 FCYLVIIRTLLQARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCEL 300
 FCYLVIIRTLLQARNFERN QLPYNGVVLAQTVANFNITSSTCEL
 Sbjct: 241 FCYLVIIRTLLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITSSTCEL 300

Query: 301 SKQLNIAVDVITYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 SKQLNIAVDVITYSLACVRCCVNPFLYAFIGVKFRND+FKLFKDLGCLSQEQLRQWSSCRH
 Sbjct: 301 SKQLNIAVDVITYSLACVRCCVNPFLYAFIGVKFRNDLFLFKDLGCLSQEQLRQWSSCRH 360

Query: 361 IRRSSMSVEAETTTTFSP 378
 IRRSSMSVEAETTTTFSP
 Sbjct: 361 IRRSSMSVEAETTTTFSP 378

 >gi|55645367|ref|XP_511477.1|  PREDICTED: chemokine (C-C motif) receptor 7 [Par
 Length = 372

Score = 669 bits (1727), Expect = 0.0

Identities = 342/372 (91%), Positives = 343/372 (92%)

Query: 7 MKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYS 66
 MKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYS
 Sbjct: 1 MKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYS 60

Query: 67 IICFXXXXXXXXXXXTYIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGV 126
 IICF TYIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGV
 Sbjct: 61 IICFVGLLGNGLVLTYYIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGV 120


Query: 127 HFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKVGSAILA 186
 HFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV G ILA
 Sbjct: 121 HFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKVGIWILA 180

Query: 187 TVLSIPELLYSGLQSSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMSF CYLVI 246
 TVLSIPELLYSGLQSSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMSF CYLVI
 Sbjct: 181 TVLSIPELLYSGLQSSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLLAMSF CYLVI 240

Query: 247 IRTLLQARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCELSKQLNI 306
 IRTLLQARNFERN QLPYNGVVLAQTVANFNITSSTCELSKQLNI
 Sbjct: 241 IRTLLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITSSTCELSKQLNI 300

Query: 307 AYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHIRRSSM 366
 AYDVTYSLACVRCCVNPFLYAFIGVKFRND+FKLFKDLGCLSQEQLRQWSSCRHIRRSSM
 Sbjct: 301 AYDVTYSLACVRCCVNPFLYAFIGVKFRNDLFLFKDLGCLSQEQLRQWSSCRHIRRSSM 360

Query: 367 SVEAETTTTFSP 378
 SVEAETTTTFSP
 Sbjct: 361 SVEAETTTTFSP 372

 >gi|56553516|gb|AAV97930.1| chemokine receptor 7 [Bos taurus]

Length = 379

Score = 635 bits (1638), Expect = 0.0

Identities = 319/379 (84%), Positives = 338/379 (89%), Gaps = 1/379 (0%)

Query: 1 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
 MDLGKPMK+VLVVALLVIFQVCLCQDEVTD+YIGDNTTVDYTL+ES+C KKDVRNFKAWF
 Sbjct: 1 MDLGKPMKNVLVVALLVIFQVCLCQDEVTDNVIGDNTTVDYTLYESVCFKKDVRNFKAWF 60

Query: 61 LPIMYSIICFXXXXXXXXXXXXTYIYFKRLKTM TD TYLLNLAVADILFLLTLPFWAYSAAK 120
 LPIMYSIICF TYIYFKRLKTM TD TYLLNL+ADILFLLTLPFWAYSAAK
 Sbjct: 61 LPIMYSIICFVGLLGNGLVMLTYIYFKRLKTM TD TYLLNLALADILFLLTLPFWAYSAAK 120






Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180
 SWVFGVH CKLIF IYK+SFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSK+
 Sbjct: 121 SWVFGVHVCKLIFGIYKISFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCL 180

Query: 181 GSAILATVLSIPELLYSDLQRSSEQAMRCSLITEHVEAFITIQVQMVIGFLVPLLAMS 240
 G +LA VLS PE++YS +Q+SSSEQA+RCSL+TEHVEA ITIQVQMV+GFL+PL+AMS
 Sbjct: 181 GIWMLAIVLSTPEVMYSGIQSSSEQALRCSLITEHVEALITIQVQMVVGFLIPLMAMS 240

Query: 241 FCYLVII RTLLQARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSST-CE 299
 FCYLVII RTLLQARNFERN QLPYNGVVLA TVANFNITS T CE
 Sbjct: 241 FCYLVII RTLLQARNFERNKAIKVIIAVVVVFVAFQLPYNGVVLAHTVANFNITS SGTSC 300

Query: 300 LSKQLNIAVDVTSYLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCR 359
 LSKQLNIAVDVTSYLACVRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQEQLRQWS CR
 Sbjct: 301 LSKQLNIAVDVTSYLACVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQEQLRQWSFCR 360

Query: 360 HIRSSMSVEAETTTTFSP 378
 H RRSSMSVEAETTTTFSP
 Sbjct: 361 HTRSSMSVEAETTTTFSP 379

 >gi|48374059|ref|NP_001001532.1|  chemokine (C-C motif) receptor 7 [Sus scrofa]
 gi|40363611|dbj|BAD06309.1|  chemokine (C-C motif) receptor 7 [Sus scrofa]
 gi|28569985|dbj|BAC57929.1|  chemokine receptor 7 [Sus scrofa]
 gi|28557110|dbj|BAC57561.1|  chemokine receptor 7 [Sus scrofa]
 Length = 380

Score = 634 bits (1635), Expect = e-180

Identities = 323/380 (85%), Positives = 337/380 (88%), Gaps = 2/380 (0%)

Query: 1 MDLGKPMK-SVLVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAW 59
 MDLGKPMK S+LVVALLVIFQVCLCQDEVTDDYIGDNTTVDYTL+ES+C KKDVR FKAW
 Sbjct: 1 MDLGKPMKKSLLVVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLYESVCFKKDVRTFKAW 60

Query: 60 FLPIMYSIICFXXXXXXXXXXXXTYIYFKRLKTM TD TYLLNLAVADILFLLTLPFWAYSAA 119
 FLP+MYSIICF TYIYFKRLKTM TD TYLLNLAVADILFLLTLPFWAYSAA
 Sbjct: 61 FLPVMYSIICFVGLLGNGLVMLTYIYFKRLKTM TD TYLLNLAVADILFLLTLPFWAYSAA 120



Query: 120 KSWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 179
 KSWVFGVH CKLIF IYK+SFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSK
 Sbjct: 121 KSWVFGVHVCKLIFGIYKISFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSK 180

Query: 180 VGSAILATVLSIPELLYSDLQRSSEQAMRCSLITEHVEAFITIQVQMVIGFLVPLLAM 239
 VG +LA VLS PELLYS Q+SSSEQA+RCSLITEHVEA ITIQVQMV+GFL+PL+AM
 Sbjct: 181 VGIWMLAMVLTSTPELLYSGTQKSSSEQALRCSLITEHVEALITIQVQMVVGFLIPLVAM 240

Query: 240 SFCYLVIIRTLQLARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAAQTVANFNITSST-C 298
 SFCYLVIIRTLQLARNFERN QLPYNGVVLAAQTVANFNITS T C
 Sbjct: 241 SFCYLVIIRTLQLARNFERNKAIKVIIAVVVVFVAFQLPYNGVVLAAQTVANFNITSGTSC 300

Query: 299 ELSKQLNIAVDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSC 358
 ELSKQLNIAVDVTYSLACVRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQE+LRQWSSC
 Sbjct: 301 ELSKQLNIAVDVTYSLACVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQERLRQWSSC 360

Query: 359 RHIRRSSMSVEAETTTTFSP 378
 RH RRSSMS EAETTTTFSP
 Sbjct: 361 RHTRSSMSAEETTTTFSP 380

 >gi|57091575|ref|XP_548131.1|  PREDICTED: similar to chemokine receptor 7 [Canis
 Length = 399

Score = 625 bits (1613), Expect = e-178
 Identities = 316/379 (83%), Positives = 333/379 (87%), Gaps = 1/379 (0%)

Query: 1 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
 M LGKPMKS+LVVALLVIFQVCLCQDEVTDDYIG+NTTVDYTL+ES+C KKDVRNFKAWF
 Sbjct: 21 MQLGKPMKSLLVVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLYESVCFKKDVRNFKAWF 80

Query: 61 LPIMYSIICFXXXXXXXXXXXXTYIYFKRLKTMDDTYLLNLAVADILFLLTLPFWAYSAAK 120
 LPIMYSIICF TYIYFKRLKTMDDTYLLNL+ADILFLLTLPFWAYSAAK
 Sbjct: 81 LPIMYSIICFMGLLGNGLVVLTYIYFKRLKTMDDTYLLNLAMADILFLLTLPFWAYSAAK 140



Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180
 SW FGVH CK+IF IYK+FFSGMLLLLCISIDRYVAIVQAVSAHRHRARVL ISKLSCV
 Sbjct: 141 SWTFGVHVCKIIFGIYKISFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLFISKLSKV 200

Query: 181 GSAILATVLSIPELLYSGLQSSSEQAAMRCSLITEHVEAFITIQVAMVIGFLVPLAMS 240
 G +LA VLS PELLYS LQ+SSSEQA+RCSL T VEA ITIQVAMV+GFL+PL AMS
 Sbjct: 201 GIWMLAMVLSPELLYSGLQSSSEQAALRCSLNTNQVEALITIQVAMVVGFLIPLGAMS 260

Query: 241 FCYLVIIRTLQLARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAAQTVANFNIT-SSTCE 299
 FCYLVIIRTLQLARNFERN QLPYNGV+LAQTVANFNIT S +CE
 Sbjct: 261 FCYLVIIRTLQLARNFERNKAIKVIIAVVVVFIAFQLPYNGVILAQTVANFNITGSGSCE 320

Query: 300 LSKQLNIAVDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCR 359
 LSKQLNIAVD+TYSLACVRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQEQLRQWSSCR
 Sbjct: 321 LSKQLNIAVDITYSLACVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQEQLRQWSSCR 380

Query: 360 HIRRSSMSVEAETTTTFSP 378
 H RRSSMSVEAETTTTFSP
 Sbjct: 381 HTRSSMSVEAETTTTFSP 399

 >gi|26332358|dbj|BAC29909.1|  unnamed protein product [Mus musculus]
 Length = 378

Score = 603 bits (1555), Expect = e-171
 Identities = 300/378 (79%), Positives = 326/378 (86%)

Query: 1 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
 MD GKP K+VLVALLVIFQVC CQDEVTDDYIG+NTTVDYTL+ES+C KKDVRNFKAWF

Sbjct: 1 MDPGKPRKNVLVALLVIFQVCFQCQDEVTDYIGENTTVDYTLYESVCFKKDVRNFKAWF 60

Query: 61 LPIMYSIICFXXXXXXXXXXXTYIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAK 120
 LP+MYS+ICF TYIYFKRLKTMTDTYLLNLAVADILFLL LPFWAYS AK

Sbjct: 61 LPLMYSVICFVGLLGNGLVILTYYIYFKRLKTMTDTYLLNLAVADILFLLILPFWAYSEAK 120

Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180
 SW+FGV+ CK IF IYK+SFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV

Sbjct: 121 SWIFGVYLCKGIFGIYKLSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180

Query: 181 GSAILATVLSIPELLYSIDLQSSSEQAMRCSLITEHVEAFITIQVQVMVIGFLVPLLAMS 240
 G +LA LSIPELLYS LQ++S E +RCSL++ VEA ITIQVQVMV GFLVP+LAMS

Sbjct: 181 GIWMLALFLSIPELLYSGLQKNSGEDTLRCSLVSQAQVEALITIQVQVMVFGFLVPLLAMS 240

Query: 241 FCYLVIIRTLLQARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCEL 300
 FCYL+IIRTLLQARNFERN QLPYNGVVLAQTVANFNIT+S+CE





Sbjct: 241 FCYLIIRTLLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITNSSCET 300

Query: 301 SKQLNIAVDVTYSLACVRCCVNPFLYAFIVGKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 SKQLNIAVDVTYSLA VRCCVNPFLYAFIVGKFR+D+FKLFKDLGCLSQE+LR WSSCRH

Sbjct: 301 SKQLNIAVDVTYSLASVRCCVNPFLYAFIVGKFRSDLFKLFKDLGCLSQERLRHWSSCRH 360

Query: 361 IRRSSMSVEAETTTTFSP 378
 +R +S+S+EAETTTTFSP

Sbjct: 361 VRNASVSMEAETTTTFSP 378

 >gi|6671772|ref|NP_031745.1|  chemokine (C-C motif) receptor 7 [Mus musculus]
 gi|468341|gb|AAA74232.1|  G protein-coupled receptor [Mus musculus]
 gi|1083330|pir|A55735 G protein-coupled receptor EBI1 - mouse
 gi|1352336|sp|P47774|CKR7 MOUSE  C-C chemokine receptor type 7 precursor (C-C CK
 (CCR-7) (MIP-3 beta receptor) (EBV-induced G
 protein-coupled receptor 1) (EBI1)
 Length = 378

Score = 601 bits (1550), Expect = e-171
 Identities = 299/378 (79%), Positives = 325/378 (85%)

Query: 1 MDLGKPMKSVLVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
 MD GKP K+VLVALLVIFQVC CQDEVTDYIG+NTTVDYTL+ES+C KKDVRNFKAWF

Sbjct: 1 MDPGKPRKNVLVALLVIFQVCFQCQDEVTDYIGENTTVDYTLYESVCFKKDVRNFKAWF 60

Query: 61 LPIMYSIICFXXXXXXXXXXXTYIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAK 120
 LP+MYS+ICF TYIYFKRLKTMTDTYLLNLAVADILFLL LPFWAYS AK

Sbjct: 61 LPLMYSVICFVGLLGNGLVILTYYIYFKRLKTMTDTYLLNLAVADILFLLILPFWAYSEAK 120

Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180
 SW+FGV+ CK IF IYK+SFFSGMLLLLCISIDRYVAIVQAVS HRHRARVLLISKLSKV

Sbjct: 121 SWIFGVYLCKGIFGIYKLSFFSGMLLLLCISIDRYVAIVQAVSRHRHRARVLLISKLSKV 180

Query: 181 GSAILATVLSIPELLYSIDLQSSSEQAMRCSLITEHVEAFITIQVQVMVIGFLVPLLAMS 240
 G +LA LSIPELLYS LQ++S E +RCSL++ VEA ITIQVQVMV GFLVP+LAMS





Sbjct: 181 GIWMLALFLSIPELLYSGLQKNSGEDTLRCSLVSQAQVEALITIQVQVMVFGFLVPLLAMS 240

Query: 241 FCYLVIIRTLLQARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCEL 300
 FCYL+IIRTLLQARNFERN QLPYNGVVLAQTVANFNIT+S+CE

Sbjct: 241 FCYLIIRTLLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITNSSCET 300

Query: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 SKQLNIAYDVTYSLA VRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQE+LR WSSCRH
 Sbjct: 301 SKQLNIAYDVTYSLASVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQERLRHWSSCRH 360

Query: 361 IRRSSMSVEAETTTTFSP 378
 +R +S+S+EAETTTTFSP
 Sbjct: 361 VRNASVSMEAETTTTFSP 378

 >gi|58477681|gb|AAH89762.1|  Chemokine (C-C motif) receptor 7 [Rattus norvegicus]
 gi|41054914|ref|NP_955783.1|  chemokine (C-C motif) receptor 7 [Rattus norvegicus]
 gi|38370235|gb|AAR24573.1|  chemokine receptor 7-like protein [Rattus norvegicus]
 Length = 378

Score = 601 bits (1549), Expect = e-170
 Identities = 297/378 (78%), Positives = 325/378 (85%)

Query: 1 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWF 60
 MDLGK K+VLVALLVIFQVC CQDEVTDYIG+NTTVDYTL+ES+C KKDVRNFKAWF
 Sbjct: 1 MDLGKPTKNVLVALLVIFQVCFCQDEVTDYIGENTTVDYTLYESVCFKKDVRNFKAWF 60

Query: 61 LPIMYSIICFXXXXXXXXXXXXXXYYIYFKRLKTMDDTYLLNLAVADILFLLTLPFWAYSAAK 120
 LP+MYS+ICF YYIYFKRLKTMDDTYLLNLAVADILFL+ LPFWAYS AK
 Sbjct: 61 LPLMYSVICFVGLLGNGLVLTYYIYFKRLKTMDDTYLLNLAVADILFLMILPFWAYSEAK 120



Query: 121 SWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180
 SW+FG + CK IF IYK+SFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV
 Sbjct: 121 SWIFGAYLCKSIFGIYKLSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSKV 180

Query: 181 GSAILATVLSIPELLYSIDLQRSSSEQAMRCSLITEHVEAFITIQVQMVGFLVPLAMS 240
 G LA LSIPELLYS LQ++S E RCSL++ VEA I IQVQMVG+GF++P+LAMS
 Sbjct: 181 GIWTLAFLLSIPELLYSGLQKNSGEDTWRCSLVSAQVEALIAIQVQMVGFLVPLAMS 240

Query: 241 FCYLVIIRTLQARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCEL 300
 FCYLVIIRTLQARNFERN QLPYNGVVLAQTVANFNIT+S+CE
 Sbjct: 241 FCYLVIIRTLQARNFERNKAIKVIIAVVVVFVQLPYNGVVLAQTVANFNITSSCEA 300

Query: 301 SKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 SKQLNIAYDVTYSLA VRCCVNPFLYAFIGVKFR+D+FKLFKDLGCLSQE+LRQWSSCRH
 Sbjct: 301 SKQLNIAYDVTYSLASVRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQERLRQWSSCRH 360

Query: 361 IRRSSMSVEAETTTTFSP 378
 +R +S+S+EAETTTTFSP
 Sbjct: 361 VRHTSVSMEAETTTTFSP 378

 >gi|50760889|ref|XP_425875.1|  PREDICTED: similar to CC chemokine receptor 7 [(
 Length = 375

Score = 421 bits (1082), Expect = e-116
 Identities = 223/370 (60%), Positives = 272/370 (73%), Gaps = 8/370 (2%)

Query: 10 VLVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYSIIC 69
 VL++ L+ F + VTDDY NTT+DY +FE +C KK+VR+F+A FLP MYS+IC
 Sbjct: 13 VLLLCRLISF---CAGNNVTDDYDA-NTTIDYNMFEMMCEKKEVRDFRAAFLPAMYSLIC 68

Query: 70 FXXXXXXXXXXXXXXYYIYFKRLKTMDDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFC 129

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      F      TYIYFKRLKTM TD YLLNLA+ADILFLLTLPFWA SAA W FG C
Sbjct: 69 FTGLLGNGLVMLTYIYFKRLKTM TDYLLNLAALADILFLLTLPFWATSAATFWCFGEFAC 128

Query: 130 KLIFAIYKMSFFSGM LLLLCISIDRYVAIVQAVSAHRHRARVLLISKLS CVGSAILATVL 189
      K ++ I KMSFFSGM LLLL ISIDRY AIVQA SAHR R R++ ISK++C+ +LA VL
Sbjct: 129 KAVYCKICKMSFFSGM LLLLSISIDRYFAIVQAASAHRRFRPRMIFISKVTCILIWLLAFVL 188

Query: 190 SIPELLYSDLQRSSSEQAMRCSLITEHVEAFIT-IQVAQM VIGFLVPLLAMSFCYLVIIR 248
      SIPEL++S + S RCS+I ++ F T I+V+QMV GFLVPL+ MS CYL+II+
Sbjct: 189 SIPELVHSGVNNYDSHP--RCSIIASDLQTFSTGIKVSQMVFGFLVPLVMSVCYLI IIK 246

Query: 249 TLLQARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCELSKQLNIAY 308
      TLLQARNFE+N QLPYNGV+LA+T++ FN TSS C+ SK+L++A
Sbjct: 247 TLLQARNFEKNAIKVIIAVVIVFVVFQLPYNGVMLAKTISVFNNNTSS-CDESKKLD MAD 305

Query: 309 DVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSV 368
      DVTY+LAC RCC+NPFLYAFIGVKFRND+FKL K+LGCLSQ++L Q SSCR +R S ++
Sbjct: 306 DVTYTLACFRCCLNPFYAFIGVKFRNDLFKLLKELGCLSQQRLWQLSSCRESKRFSFAM 365

Query: 369 EAETTTTFSP 378
      E ETTTTFSP
Sbjct: 366 ETETTTTFSP 375

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 >gi|33415854|gb|AAQ18436.1|  chemokine receptor 7 [Bos taurus]
Length = 246

Score = 409 bits (1050), Expect = e-113

Identities = 210/247 (85%), Positives = 222/247 (89%), Gaps = 2/247 (0%)

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Query: 133 FAIYKMSFFSGM LLLLCISIDRYVAIVQAVSAHRHRARVLLISKLS CVGSAILATVLSIP 192
      FAIYKMSFFSGM LLL CISIDRYVAIVQAVSAHRHRARVLLISKLS C+G +LA VLS P
Sbjct: 1 FAIYKMSFFSGM LLL-CISIDRYVAIVQAVSAHRHRARVLLISKLSCLGIWMLAIVLSTP 59

Query: 193 ELLYSDLQRSSSEQAMRCSLITEHVEAFITIQVAQM VIGFLVPLLAMSFCYLVIIR TLLQ 252
      E++YS +Q+SSSEQA+RCSL+TEHVEA ITIQVAQMV+GFL+PL+AMSF CYLVIIR TLLQ
Sbjct: 60 EVMYSGIQKSSSEQALRCSLVTEHVEALITIQVAQMVVGFLIPLMAMSF CYLVIIR TLLQ 119

Query: 253 ARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSST-CELSKQLNIAYDVT 311
      ARNFERN QLPYNGVVLAQTVANFNITS T CELSKQLNIAYDVT
Sbjct: 120 ARNFERNKAIKVIIAVVVVFVAFQLPYNGVVLAQTVANFNITSGTSCELSKQLNIAYDVT 179

Query: 312 YSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVEAE 371
      YSLACVRCCVNPFLYAFIGVKFRND+FKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVEAE
Sbjct: 180 YSLACVRCCVNPFLYAFIGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVEAE 239

Query: 372 TTTTFSP 378
      TTTTFSP
Sbjct: 240 TTTTFSP 246

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 >gi|49118818|gb|AAH73273.1|  MGC80638 protein [Xenopus laevis]
Length = 358

Score = 375 bits (963), Expect = e-102

Identities = 186/364 (51%), Positives = 251/364 (68%), Gaps = 7/364 (1%)

Query: 16 LVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFXXXXX 75
 + FQ+ + +D V+ D +T+DY+ +++C K DVR F++ FLP MY+IIC
 Sbjct: 1 MATFQLAVGEDNVSTDENVPYSTMDYSDLQTVQCQKGDVTRFRSSFLPAMYTIICLVGLAG 60

Query: 76 XXXXXXTYIYFKRLKTMDDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFKLIFAI 135
 Y+YF RLK TD Y+LNLA+ADI+FLLTLPFWA S AK+WVFG CK+I+ +
 Sbjct: 61 NGLVMIRYLYFNRLKNGTDYMLNLAIADIVFLLTLPFWAVSVAKNWVFGSEMCKIIYCL 120

Query: 136 YKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELL 195
 YKMSFFSGM LL+C+S++RY AIVQA SAHRHR++ +LISKLS +G + A +LSIPELL
 Sbjct: 121 YKMSFFSGMFLLMCVSMERYFAIVQAPSARHRRSKTVLISKLSLGIWVFAFLLSIPELL 180

Query: 196 YSDLQRSSEQAMRCSLITEHVEAF-ITIQVQMVGFLVPLLAMSFCYLVIIRTLLQAR 254
 YS + + C + + +++ +++++QM GF +PL+ M+ CY +IIR LLQAR
 Sbjct: 181 YSGVNNNGG--VNMCIIFSNSIQSLSAKLKISQMFFGFFLPLIIMALCYCMIIRKLLQAR 238

Query: 255 NFERNXXXXXXXXXXXXXXXXXQLPYNGVLAQTVANFNITSSTCELSKQLNIAYDVTYSL 314
 NFE+ QLPYN V+L +T N + CE SK+L+IA DVTYSL
 Sbjct: 239 NFEKYKAIKVIAIVIVFVAFQLPYNSVMLIKTFDN----GTDCEASKKLDIADDVTYSL 294

Query: 315 ACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVEAETTT 374
 AC RCC+NPFLYA IG+KFRND+ KLFKD+GCLSQE++ +WSS + RR+S +++ ETTT
 Sbjct: 295 ACFRCCLNPFLYAIIGIKFRNDLCKLFKDIGCLSQEKITEWSSAKPSRRTSFAMDTETTT 354

Query: 375 TFSP 378
 TFSP
 Sbjct: 355 TFSP 358

☐ >gi|47223975|emb|CAG06152.1| unnamed protein product [Tetraodon nigroviridis]
 Length = 848

Score = 286 bits (731), Expect = 9e-76

Identities = 149/339 (43%), Positives = 205/339 (60%), Gaps = 9/339 (2%)

Query: 38 TVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFXXXXXXXXXXXXTYIYFKRLKTMDDTYL 97
 T DY+ F ++C K+ R F+ WF+P YS+I F T+ YFKRLKTMDD YL
 Sbjct: 1 TADYSTFPFTVCVKELNRQFRRWFMPFTFYSVIFFLGLAGNLLVILTFYFKRLKTMDDVYL 60

Query: 98 LNLAVADILFLLTLPFWAYSAAKSWVFGVHFKLIFAIYKMSFFSGMLLLLCISIDRYVA 157
 LNL+ AD+LF L+LPFWA + WV G C ++ +YK+SF+S M LL CIS+DRY A
 Sbjct: 61 LNLAFADLLFALSPLFWAANTMTKWVLGEEMCIAMYTVMYKVSFYSSMFLCCISVDRYFA 120

Query: 158 IVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRSSEQAMRCSLITEHV 217
 I +A SA+R+R++ + +SK+S + A + S+PE+ Y+ + ++ C+ T
 Sbjct: 121 ISKATSAYRYSQTMFLSKVSSAVVWVAALIFSMPEMRYTSVNNNT-----CTPYTGSK 174

Query: 218 EAF-ITIQVQMVGFLVPLLAMSFCYLVIIRTLLQARNFERNXXXXXXXXXXXXXXXXXQ 276
 + + IQV Q+V+ F +PL+ MS CY II+TL QA+NERN Q
 Sbjct: 175 DQLRVIIQVGQIVLAFALPLVIMSICYSSIIKTLCAQNERNKAIKVLAVVAVFLVSQ 234

Query: 277 LPYNGVLAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRND 336
 +PYN V+ T+ +++C L A DVT LA RCC+NP +YAFIGVKFRND
 Sbjct: 235 VPYNLVLFWSTLVTAAGGTTSCSYDNLLYATDVTQCLAFFRCCLNPIVYAFIGVKFRND 294

Query: 337 IFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVEAETTTT 375
 + KL KD GC+S E +++S R RRSS E ETTT
 Sbjct: 295 LLKLLKDWGCMSESFFKYTSRR--RRSSGFTETETTTT 331

>gi|14043042|ref|NP_112477.1| **G** chemokine (C-C motif) receptor 9 isoform A [Homo
 gi|46854634|gb|AAH69678.1| **G** Chemokine (C-C motif) receptor 9, isoform A [Homo sa
 gi|7673009|gb|AAF66699.1| **G** CC chemokine receptor 9A [Homo sapiens]
 gi|4886432|emb|CAB43477.1| **G** chemokine receptor CCR9 [Homo sapiens]
 Length = 369

Score = 251 bits (641), Expect = 2e-65

Identities = 128/335 (38%), Positives = 198/335 (59%), Gaps = 16/335 (4%)

Query: 28 VTDDYIGDNTT-----VDYTLFESLCSKDVDNRNFKAWFLPIMYSIICFXXXXXXXXXXXXXT 82
 + DDY ++T+ V++ + C K +VR F + FLP +Y ++
 Sbjct: 13 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 72

Query: 83 YIYFKRLKTM TD TYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFS 142
 Y Y R+KTMTD +LLNLA+AD+LFL+TLPFWA +AA W F CK++ ++YKM+F+S
 Sbjct: 73 YWYCTRVKTM TDMFLNLAIADLLFLVTLFPWAIAAADQWKQTFMCKVVNSMYKMFYS 132

Query: 143 GMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSVGSAILATVLSIPELLYSDLQRS 202
 +LL++CIS+DRY+AI QA+ AH R + LL SK+ C +LA L IPE+LYS ++
 Sbjct: 133 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWLAAALCIPEILYSQIKEE 192

Query: 203 SSEQAMRCSLI-----TEHVEAFITIQVAQMVGFLVPLLAMSF CYLVIIRTLQARNF 256
 S C+++ T+ A +T++V ++GF +P + M+ CY +II TL+QA+
 Sbjct: 193 SG--IAICTMVYPSDESTKLKSAVLT LKV---ILGFFLPFVVMACCYTIIHTLIQAKKS 247

Query: 257 ERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQT VANFNITSSTCELSKQLNIAVDV TYSLAC 316
 ++ Q PYN ++L QT+ + + S C +S ++I + VT ++A
 Sbjct: 248 SKHKALKVTITVLT VFLVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 307

Query: 317 VRCCVNPFYAFIGVKFRNDIFKLFKDLGCLS QEQ 351
 C+NP LY F+G +FR D+ K K+LGC+SQ Q
 Sbjct: 308 FHSCINPVLYVFGVGERFRRDLVKT LKNLGCISQAQ 342

>gi|14043044|ref|NP_006632.2| **G** chemokine (C-C motif) receptor 9 isoform B [Homo
 gi|29825379|gb|AAO92294.1| **G** chemokine (C-C motif) receptor 9 [Homo sapiens]
 gi|7673011|gb|AAF66700.1| **G** CC chemokine receptor 9B [Homo sapiens]
 gi|1245055|gb|AAA93319.1| **G** GPR-9-6
 gi|1730237|sp|P51686|CKR9 HUMAN **G** C-C chemokine receptor type 9 (C-C CKR-9) (CC-C
 (GPR-9-6)
 Length = 357

Score = 251 bits (641), Expect = 2e-65

Identities = 128/335 (38%), Positives = 198/335 (59%), Gaps = 16/335 (4%)

Query: 28 VTDDYIGDNTT-----VDYTLFESLCSKDVDNRNFKAWFLPIMYSIICFXXXXXXXXXXXXXT 82
 + DDY ++T+ V++ + C K +VR F + FLP +Y ++
 Sbjct: 1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60

Query: 83 YIYFKRLKTM TD TYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFS 142
 Y Y R+KTMTD +LLNLA+AD+LFL+TLPFWA +AA W F CK++ ++YKM+F+S
 Sbjct: 61 YWYCTRVKTM TDMFLNLAIADLLFLVTLFPWAIAAADQWKQTFMCKVVNSMYKMFYS 120

Query: 143 GMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSVGSAILATVLSIPELLYSDLQRS 202

+LL++CIS+DRY+AI QA+ AH R + LL SK+ C +LA L IPE+LYS ++
 Sbjct: 121 CVLLIMCISVDRIYIAIAQAMRAHTWREKRLLYSKMVCFTIWLAAALCIPEILYSQIKEE 180
 Query: 203 SSEQAMRCSLI-----TEHVEAFITIQVQMVGFLVPLLAMSF CYLVIIRTLQARNF 256
 S C+++ T+ A +T++V ++GF +P + M+ CY +II TL+QA+
 Sbjct: 181 SG--IAICTMVYPSESTKLKSAVLTLLKV---ILGFFLPFVVMACCYTIIHTLIQAKKS 235
 Query: 257 ERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCELSKQLNIAVDVTVSLAC 316
 ++ Q PYN ++L QT+ + + S C +S ++I + VT ++A
 Sbjct: 236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
 Query: 317 VRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQQ 351
 C+NP LY F+G +FR D+ K K+LGC+SQ Q
 Sbjct: 296 FHSCLPVLYVFGFRDRLVKTLKNLGCISQAQ 330

>gi|57101682|ref|XP_541909.1| **G** PREDICTED: similar to chemokine (C-C motif) rece
 [Canis familiaris]
 Length = 642

Score = 250 bits (639), Expect = 4e-65
 Identities = 137/372 (36%), Positives = 208/372 (55%), Gaps = 15/372 (4%)

Query: 8 KSVLVVALLVIFQVCLCQDEVTDYIGDNTTV--DYTLFESL-CSKKDVRNFKAWFLPIM 64
 K + +++V + ++DDY +T+ DY F L C K VR F + FLP +
 Sbjct: 268 KQACIWSIMVPTEFTNLISNISDDYSYHSTSPVDDYMNFPDLFCQKGHVRQFASHFLPPL 327
 Query: 65 YSIICFXXXXXXXXXXTYIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVF 124
 Y ++ Y Y R+KTMTD +LLNLA+AD+LFL TLPFWA +AA W F
 Sbjct: 328 YWLVFIVGTGLNSLVILVYCYCTRVKTMMDMFLNLAIADLLFLLTLPFWAIAAADQWKF 387
 Query: 125 GVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSVGSAL 184
 CK++ ++YKM+F+S +LL++CIS+DRY+AI QA A R + L+ SK+ C +
 Sbjct: 388 QTPCLKVNSMYKMFYSCVLLIMCISVDRIYIAIAQATKAQTWRQKRLVYSKMVCFTVWV 447
 Query: 185 LATVLSIPELLYSIDLQRSSEQAMRCSLI---TEHVEAFITIQVQMVGFLVPLLAMSF 241
 +A L IPELLYS L+ S C+++ ++ + + ++++GF +P + M+
 Sbjct: 448 VAATLCIPELLYSQLKEES--DITICTMVYPSDQNSKVKSVVLTLLKVILGFFLPFVVMAC 505
 Query: 242 CYLVIIRTLQARNFERNXXXXXXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSTCELS 301
 CY +II TLLQAR ++ Q PYN ++L QT+ + + S C +S
 Sbjct: 506 CYTIIYTLQARKSSKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYTVFLSNCAIS 565
 Query: 302 KQLNIAVDVTVSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQQQLRQWSSCRH- 360
 ++I + VT ++A C+NP LY F+G +FR D+ K K LGC+SQE QW S
 Sbjct: 566 TNVDICFQVTQTIAFFHSCLPVLYVFGFRDRLVKTLKSLGCISQE---QWVSFTRR 622
 Query: 361 ---IRRSSMSVE 369
 ++ SSM +E
 Sbjct: 623 EGSVKLSSMLE 634

>gi|6753462|ref|NP_034043.1| **G** chemokine (C-C motif) receptor 9 [Mus musculus]
 gi|4886533|emb|CAB43460.1| **G** chemokine receptor CCR9 [Mus musculus]
 gi|7159932|emb|CAB66136.2| **G** CCR9 chemokine receptor [Mus musculus]
 gi|26341364|dbj|BAC34344.1| **G** unnamed protein product [Mus musculus]

gi|12859710|dbj|BA331747.1| [G] unnamed protein product [Mus musculus]
 gi|8134364|sp|Q9WUT7|CKR9 MOUSE [G] C-C chemokine receptor type 9 (C-C CKR-9) (CC-C
 (Chemokine C-C receptor 10)
 Length = 369

Score = 247 bits (631), Expect = 3e-64
 Identities = 124/326 (38%), Positives = 192/326 (58%), Gaps = 11/326 (3%)

Query: 29 TDDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFXXXXXXXXXXXXTYIYFKR 88
 TDDY+ N + + C K +VR F + FLP +Y ++ Y Y R
 Sbjct: 25 TDDYMNLNFSFFF-----CKKNVRQFASHFLPPLYWLVFIVGTLGNSLVILVYWYCTR 78

Query: 89 LKTMTDITYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGMLLLL 148
 +KTMTD +LLNLA+AD+LFL TLPFWA +AA W+F CK++ ++YKM+F+S +LL++
 Sbjct: 79 VKTMTDMFLNLAIADLLFLATLPFWAIAAAGQWMEQTFMCKVVNSMYKMFYSCVLLIM 138

Query: 149 CISIDRYVAIVQAVSAHRHRARVLLISKLSVGSAILATVLSIPELLYSDLRSSSEQAM 208
 CIS+DRY+AIVQA+ A R + LL SK+ C+ ++A VL PE+LYS Q S
 Sbjct: 139 CISVDRYIAIVQAMKAQVWRQKRLLYSKMVCITIWVMAAVLCTPEILYS--QVSGESGIA 196

Query: 209 RCSLI---TEHVEAFITIQVQVMVIGFLVPLLAMSFCYLVIIIRTLLQARNFERNXXXXXX 265
 C+++ ++ + + + ++ +GF +P + M+FCY +II TL+QA+ ++
 Sbjct: 197 TCTMVYPKDKNAKLKSAVLILKVTLGFFLPFMVMAFCYTIIHTLVQAKKSSKHKALKVT 256

Query: 266 XXXXXXXXXXXXQLPYNGVVLQQTVANFNITSSSTCELSKQLNIAVDVTYSLACVRCCVNPFL 325
 Q PYN +++ Q V + + S C +S ++I + VT ++A C+NP L
 Sbjct: 257 ITVLTVFIMSQFPYNSILVVQAVDAYAMFISNCTISTNIDICFQVTQTIAFFHSCLNPVL 316

Query: 326 YAFIGVKFRNDIFKLFKDLGCLSQQEQ 351
 Y F+G +FR D+ K K+LGC+SQ Q
 Sbjct: 317 YVFVGERFRRLVKTLLKLGICISQAQ 342

>gi|27229230|ref|NP_758832.1| [G] chemokine (C-C motif) receptor 9 [Rattus norvegicus]
 gi|25991905|gb|AA76989.1| [G] chemokine receptor CCR9 [Rattus norvegicus]
 Length = 369

Score = 247 bits (630), Expect = 4e-64
 Identities = 127/330 (38%), Positives = 193/330 (58%), Gaps = 10/330 (3%)

Query: 30 DDYIGDNT--TVDY---TLFESLCSKKDVRNFKAWFLPIMYSIICFXXXXXXXXXXXXTYI 84
 DDY D+T T DY C K +VR F + FLP +Y ++ Y
 Sbjct: 15 DDYSYDSTASTDDYMNLNFSFFCKKNVRQFASHFLPPLYWLVFVVGTVGNSLVILVYW 74

Query: 85 YFKRLKTMTDITYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGM 144
 Y R+KTMTD +LLNLA+AD+LFL TLPFWA +AA W+F CK++ ++YKM+F+S +
 Sbjct: 75 YCTRVKTMDFLLNLAIADLLFLATLPFWAIAAAGQWMEQTFMCKVVNSMYKMFYSCV 134

Query: 145 LLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSVGSAILATVLSIPELLYSDLRSSS 204
 LL++CIS+DRY+AIVQA+ A R + LL SK+ C+ ++A VL PE+LYS Q S
 Sbjct: 135 LLIMCISVDRYIAIVQAMKAQVWRQKRLLYSKMVCITIWVMAAVLCTPEILYS--QISGE 192

Query: 205 EQAMRCSLI---TEHVEAFITIQVQVMVIGFLVPLLAMSFCYLVIIIRTLLQARNFERNXX 261
 C+++ ++ + + + ++ +GF +P + M+FCY +II TL+QA+ ++
 Sbjct: 193 SGIAICTMVYPKDKNAKLKSAVLILKVTLGFFLPFMVMAFCYTIIHTLVQAKKSSKHKA 252





Query: 262 XXXXXXXXXXXXQLPYNGVVLQQTVANFNITSSSTCELSKQLNIAVDVTYSLACVRCCV 321
 Q PYN +++ Q V + + S C +S ++I + VT ++A C+

Sbjct: 253 LKVTITVLTVFIMSQFPYNCILVVQAVDAYTMFISNCTISTNIDICFQVTQTIAFFHSCL 312

Query: 322 NPFLYAFIGVKFRNDIFKLFKDLGCLSSEQ 351

NP LY F+G +FR D+ K K+LGC+SQ Q

Sbjct: 313 NPVLYVVFVGERFRRDLVKTLKNLGCISQAQ 342

 >gi|48675913|ref|NP_001001624.1|  chemokine C-C motif receptor 9 [Sus scrofa]
 gi|44890862|dbj|EAD12126.1|  chemokine C-C motif receptor 9 [Sus scrofa]
 gi|41688289|dbj|EAD08643.1|  chemokine (C-C motif) receptor 9 isoform A [Sus scr
 Length = 369

Score = 245 bits (626), Expect = 1e-63

Identities = 130/333 (39%), Positives = 191/333 (57%), Gaps = 16/333 (4%)

Query: 30 DDYIGDNTTV-----DYTLFESLCSKKDVRNFKAWFLPIMYSIICFXXXXXXXXXXXXXTYI 84
 DDY D T ++T + C K VR F + FLP +Y ++ Y

Sbjct: 15 DDYGYDATPSIEDYGNFTFTDLFCKKNHVRQFASHFLPPLYWLVFIVGAVGNSLVILVYW 74

Query: 85 YFKRLKTMTDITYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGM 144
 Y R+KTMTD +LLNLA+AD+LFL+TLPFWA +AA W F CK++ ++YKM+F+S +

Sbjct: 75 YCTRVKTMMDMFLNLAIADLLFLVTLPFWAIAAADQWKFTFMCKVVNSMYKMFYSCV 134

Query: 145 LLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSVGSAILATVLSIPELLYSDLRSSS 204
 LL++CIS+DRY+AI QA+ A R + LL SKL C ++A L IPELLYS Q

Sbjct: 135 LLIMCISVDRIYIAIAQAMRAQTWRQKRLLYSKLVCFTVWVMAAALCIPELLYS--QVKEE 192

Query: 205 EQAMRCSLI-----TEHVEAFITIQVQMVGFLVPLLAMSFCYLVIIIRTLQARNFER 258
 C+++ T A +T++V ++GF +P + M+ CY +II TL+QA+ +

Sbjct: 193 HDIAICTMVYPSDESTNLKSAVLTCLKV---ILGFFLPFVVMACCYTIIHTLIQAKKSSK 249



Query: 259 NXXXXXXXXXXXXXXXXXQLPYNGVVLQAQTVANFNITSSTCELSKQLNIAVDVYSLACVR 318
 + Q PYN V+L QT+ + + S+C +S ++I + VT ++A

Sbjct: 250 HKALKVTITVLTVFVLSQFPYNCVLLVQTIDAYTMFISSCAVSTNIDICFQVTQTIAFFH 309

Query: 319 CCVNPFLYAFIGVKFRNDIFKLFKDLGCLSSEQ 351

C+NP LY F+G +FR D+ K K+LGC+SQ Q

Sbjct: 310 SCLNPVLYVVFVGERFRRDLVKTLKNLGCISQAQ 342

 >gi|41688290|dbj|EAD08644.1|  chemokine (C-C motif) receptor 9 isoform B [Sus :
 Length = 357

Score = 245 bits (626), Expect = 1e-63

Identities = 130/333 (39%), Positives = 191/333 (57%), Gaps = 16/333 (4%)

Query: 30 DDYIGDNTTV-----DYTLFESLCSKKDVRNFKAWFLPIMYSIICFXXXXXXXXXXXXXTYI 84
 DDY D T ++T + C K VR F + FLP +Y ++ Y

Sbjct: 3 DDYGYDATPSIEDYGNFTFTDLFCKKNHVRQFASHFLPPLYWLVFIVGAVGNSLVILVYW 62

Query: 85 YFKRLKTMTDITYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGM 144
 Y R+KTMTD +LLNLA+AD+LFL+TLPFWA +AA W F CK++ ++YKM+F+S +

Sbjct: 63 YCTRVKTMMDMFLNLAIADLLFLVTLPFWAIAAADQWKFTFMCKVVNSMYKMFYSCV 122



Query: 145 LLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSVGSAILATVLSIPELLYSDLRSSS 204
 LL++CIS+DRY+AI QA+ A R + LL SKL C ++A L IPELLYS Q

Sbjct: 123 LLIMCISVDRIYIAIAQAMRAQTWRQKRLLYSKLVCFTVWVMAAALCIPELLYS--QVKEE 180

Query: 205 EQAMRCSLI-----TEHVEAFITIQVAQMVGFLVPLLAMSFCYLVIIRTLLQARNFER 258
 C+++ T A +T++V ++GF +P + M+ CY +II TL+QA+ +
 Sbjct: 181 HDIAICTMVYPSDESTNLKSAVLTALKV---ILGFFLPFVVMACCYTIIHTLIQAKKSSK 237

Query: 259 NXXXXXXXXXXXXXXXXXQLPYNGVVLQAQTVANFNITSSTCELSKQLNIAVDVYSLACVR 318
 + Q PYN V+L QT+ + + S+C +S ++I + VT ++A
 Sbjct: 238 HKALKVTITVLTVFVLSQFPYNCVLLVQTIDAYTMFISSCAVSTNIDICFQVTQTIAFFH 297

Query: 319 CCVNPFLYAFIVGKFRNDIFKLFKDLGCLSSEQ 351
 C+NP LY F+G +FR D+ K K+LGC+SQ Q
 Sbjct: 298 SCLNPVLYVFGFRDLVKTLKNLGCISQAQ 330

 >[gi|34853814|ref|XP_217862.2|](#)  similar to G protein-coupled receptor KY411 [Rat]
 Length = 509

Score = 231 bits (590), Expect = 2e-59
 Identities = 131/355 (36%), Positives = 201/355 (56%), Gaps = 13/355 (3%)

Query: 35 DNTTVDYTLFESL--CSKKDVRNFKAWFLPIMYSIICFXXXXXXXXXXTYIYFKRLKTM 92
 D T DY++F CS ++VR+F F+PI YS+IC T+ ++K+ ++M
 Sbjct: 155 DYTGSDYSMPETEPESLQEVDFTKVFPIAYSLICVFGLLGNNIMVITFAFYKKARSM 214



Query: 93 TDTYLLNLAVADILFLLTLPLFWAYS-AAKSWVFGVHFCKLIFAIYKMSFFSGMLLLLCIS 151
 TD YLLN+A+ DILF+LTLPFWA + A +W+FG CKL+ Y ++F GMLLL CIS
 Sbjct: 215 TDVYLLNMAITDILFVLTLPFWAVTHATDTWIFGNTMCKLMKGTAVNFNCGMLLLACIS 274

Query: 152 IDRYVAIVQAVSAHRHRARVLLISKLSVGSAILATVLSIPELLYSDLQSSSEQAM--R 209
 +DRY+AIVQA + R R+R L SK+ C+ ++ ++S P ++ + +
 Sbjct: 275 MDRYIAIVQATKSFRVRSRTLTHSKVICLTWVFSIISSPTFFFNKQYKLQGRDVCEPQ 334

Query: 210 CSLITEHVEAFITIQVAQMVGFLVPLLAMSFCYLVIIRTLLQARNFERNXXXXXXXXXX 269
 L++E + + +++ GF +PLL M FCYL II+TL+QA+N +R+
 Sbjct: 335 YKLVSPEITWKLGLGMLLELFGFFIPLLEMFVFCYLFIIKTLVQAQNSKRHRRAIRVVIADV 394

Query: 270 XXXXXQLPYNGVVLQAQTVANFNITSSTCELSKQLNIAVDVYSLACVRCCVNPFLYAFI 329
 Q+P+N +VL T AN +C K L A +V LA + CC+NP LYAFI
 Sbjct: 395 LVFLACQIPHNLVLLVTAANTGKMGRSCSAEKALAYARNVAEVLAFHCCCLNPVLYAFI 453

Query: 330 GVKFRNDIFKLFKDLGCLSSEQ-----LRQWSSCRHIRRSSMSVEAETTTTFS 377
 G KFR+ K+ KD+ C+ ++ R +S R++S +VE + ++F+
 Sbjct: 454 GQKFRSYFMKIMKDVCMRRKSKVPTFFCARVYSESYISQTSQTVENDNASSFT 508

 >[gi|1668738|emb|CAB02144.1|](#)  G PROTEIN-COUPLED RECEPTOR CKR-L3 [Homo sapiens]
[gi|2135142|pir|JC5068](#) G protein-coupled receptor CKR-L3 - human
 Length = 369

Score = 229 bits (584), Expect = 1e-58
 Identities = 130/352 (36%), Positives = 198/352 (56%), Gaps = 8/352 (2%)

Query: 29 TDDYIGDNTTVDYTLFES--LCSKKDVRNFKAWFLPIMYSIICFXXXXXXXXXXTYIYF 86
 ++DY T Y++ LCS ++VR F F+PI YS+IC T+ ++
 Sbjct: 10 SEDYFVSVNTSYYSVDSEMLLCSLQEVRFQSRLEFVPIAYSLICVFGLLGNNILVVITFAFY 69

Query: 87 KRLKTMDDTYLLNLAVADILFLLTLPLFWAYS-AAKSWVFGVHFCKLIFAIYKMSFFSGML 145

K+ ++MTD YLLN+A+ADILF+LTLPEFWA S A +WVF CKL+ IY ++F GML
 Sbjct: 70 KKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINFNCGML 129

Query: 146 LLLCISIDRYVAIVQAVSAHRHRARVLLISKLSVGSAILATVLSIPELLYSDLQRSSSE 205
 LL CIS+DRY+AIVQA + R R+R L SK+ C+ L+ ++S +++ +
 Sbjct: 130 LLTCISMDRYIAIVQATKSFRLRSRTLPRSKIICLVVWGLSVIISSTFVFNQKYNTQGS 189

Query: 206 QAM--RCSLITEHVEAFITIQVQVMVIGFLVPLLAMSFCYLVIIRTLLQARNFERNXXXX 263
 + ++E + + + +++ GF +PL+ M FCY I++TL+QA+N +R+
 Sbjct: 190 DVCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLFMIFCYTFIVKTLVQAQNSKRHKAIR 249

Query: 264 XXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSSTCELSKQLNIAVDVTYSLACVRCCVNP 323
 Q+P+N +VL T AN + +C+ K + VT LA + CC+NP
 Sbjct: 250 VIIAVVLVFLACQIPHNL-MVLLVTAANLGMNRSCQSEKLIGYTKTVTEVLAFLHCCLNP 308

Query: 324 FLYAFIGVKFRNDIFKLFKDLGCLSQEQLRWSSCRHIRRSSMSVEAETTTT 375
 LYAFIG KFRN K+ KDL C+ ++ SC R S ++ +T+ T
 Sbjct: 309 VLYAFIGQKFRNYFLKILKDLWCVRKYKSSGFSC--AGRYSENISRQTSET 358

>gi|37188165|ref|NP_113597.2| G chemokine (C-C motif) receptor 6 [Homo sapiens]
 gi|37187860|ref|NP_004358.2| G chemokine (C-C motif) receptor 6 [Homo sapiens]
 gi|29825375|gb|AA092293.1| G chemokine (C-C motif) receptor 6 [Homo sapiens]
 gi|23272703|gb|AAH37960.1| G Chemokine (C-C motif) receptor 6 [Homo sapiens]
 gi|9453791|emb|CAB99328.1| G GD:CCR6 [Homo sapiens]
 gi|2251211|gb|AAB62714.1| G GPR-CY4
 gi|2851567|sp|P51684|CKR6 HUMAN G C-C chemokine receptor type 6 (C-C CKR-6) (CC-C
 receptor) (GPR-CY4) (GPCY4) (Chemokine receptor-like 3)
 (CKR-L3) (DRY6)
 Length = 374

Score = 229 bits (584), Expect = 1e-58

Identities = 130/352 (36%), Positives = 198/352 (56%), Gaps = 8/352 (2%)

Query: 29 TDDYIGDNTTVDYTLFES--LCSKDVNRNFKAWFLPIMYSIICFXXXXXXXXXXXXTYIYF 86
 ++DY T Y++ LCS ++VR F F+PI YS+IC T+ ++
 Sbjct: 15 SEDYFVSVNTSYYSVDSEMLLCSLQEVQRQSRFLVPIAYSLLICVFGLLGNILVVITFAFY 74

Query: 87 KRLKTMDDTYLLNLAVADILFLLTLPFWAYS--AAKSWVFGVHFCKLIFAIYKMSFFSGML 145
 K+ ++MTD YLLN+A+ADILF+LTLPEFWA S A +WVF CKL+ IY ++F GML
 Sbjct: 75 KKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINFNCGML 134

Query: 146 LLLCISIDRYVAIVQAVSAHRHRARVLLISKLSVGSAILATVLSIPELLYSDLQRSSSE 205
 LL CIS+DRY+AIVQA + R R+R L SK+ C+ L+ ++S +++ +
 Sbjct: 135 LLTCISMDRYIAIVQATKSFRLRSRTLPRSKIICLVVWGLSVIISSTFVFNQKYNTQGS 194

Query: 206 QAM--RCSLITEHVEAFITIQVQVMVIGFLVPLLAMSFCYLVIIRTLLQARNFERNXXXX 263
 + ++E + + + +++ GF +PL+ M FCY I++TL+QA+N +R+
 Sbjct: 195 DVCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLFMIFCYTFIVKTLVQAQNSKRHKAIR 254

Query: 264 XXXXXXXXXXXXXQLPYNGVVLAQTVANFNITSSSTCELSKQLNIAVDVTYSLACVRCCVNP 323
 Q+P+N +VL T AN + +C+ K + VT LA + CC+NP
 Sbjct: 255 VIIAVVLVFLACQIPHNL-MVLLVTAANLGMNRSCQSEKLIGYTKTVTEVLAFLHCCLNP 313

Query: 324 FLYAFIGVKFRNDIFKLFKDLGCLSQEQLRWSSCRHIRRSSMSVEAETTTT 375
 LYAFIG KFRN K+ KDL C+ ++ SC R S ++ +T+ T
 Sbjct: 314 VLYAFIGQKFRNYFLKILKDLWCVRKYKSSGFSC--AGRYSENISRQTSET 363

>gi|47221187|emb|CAG05508.1| unnamed protein product [Tetraodon nigroviridis]
Length = 277

Score = 229 bits (584), Expect = 1e-58

Identities = 117/252 (46%), Positives = 164/252 (65%), Gaps = 2/252 (0%)

Query: 88 RLKTM TD TYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGM LLL 147
RLKTM TD YLLNLAVAD+LFL TLPF A A K W FG+ CK + A+Y+++FFSGM LLL
Sbjct: 23 RLKTM TDVYLLNLAVADLLFLCTLPFLAVEAIKYWNFGLALCKTVLAVYRINFFSGM LLL 82

Query: 148 LCISIDRYVAIVQAVSAHRHRARVLLISKLS CVGSAILATVLSIPELLYSDLQRSSEQA 207
CIS+DRY++IVQ A + + L SKL C+ +++T+L++PE +Y+ ++ +Q+
Sbjct: 83 TCISVDRIYISIVQVTKAQNTKKQRLFW SKLICLIVVWVSTLLALPEFIYARVKTQ RDQS 142

Query: 208 MRCSLITEHVEAFITIQV--AQMVIGFLVPLLAMSFCYLVIIR TLLQARNFERNXXXXXX 265
+ + ++ E I I V Q+ +GF +PL+ M FCY V+IR TLLQARNF+++
Sbjct: 143 LCTLIYWDNSENQIKILVLSIQICMGFWLPLMVMIFCYSVVIR TLLQARNFQKH KALRVI 202

Query: 266 XXXXXXXXXXXXQLPYNGV VLAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNPFL 325
QLPYN +++ +T N T S+CE L +A +T SLA C+NPFL
Sbjct: 203 FAVVLV FVLSQLPYNSLLIFETTQAANTMSSCETRINLELAKQITKSLAYAHACLNPFL 262

Query: 326 YAFIGVKFRNDI 337
YAFIGV+FR D+
Sbjct: 263 YAFIGVRFRQDL 274

>gi|55627742|ref|XP_527565.1| **G** PREDICTED: chemokine (C-C motif) receptor 6 [Par]
Length = 522

Score = 228 bits (582), Expect = 2e-58

Identities = 130/352 (36%), Positives = 197/352 (55%), Gaps = 8/352 (2%)

Query: 29 TDDYIGDN TTVDYTLFES--LCSKKDVRNFKAWFLPIMYSIICFXXXXXXXXXXXXXTYIYF 86
++DY T Y++ LCS ++VR F F+PI YS+IC T+ ++
Sbjct: 163 SEDYFVSVNTSYYSVDSETLLCSLQEV RQFSRLFVPIAYSLICVFGLLG NILVVITFAFY 222

Query: 87 KRLKTM TD TYLLNLAVADILFLLTLPFWAYSAAKS-WVFGVHFCKLIFAIYKMSFFSGM L 145
K+ ++MTD YLLN+A+ADILF+LTLPFWA S A WVF CKL+ IY ++F GML
Sbjct: 223 KKARSMTDVYLLNMAIADILFVL TLPFWAVSHATGVWVFSNATCKLLKGIYAINFCGML 282

Query: 146 LLLCISIDRYVAIVQAVSAHRHRARVLLISKLS CVGSAILATVLSIPELLYSDLQRSSE 205
LL CIS+DRY+AIVQA + R R+R L SK+ C+ L+ ++S +++ +
Sbjct: 283 LLTCISMDRYIAIVQATKSFR LRSRTLPRSKIICLVVWGLSVIISSTFVFNQKYNTQGS 342

Query: 206 QAM--RCSLITEHVEAFITIQVAQMVIGFLVPLLAMSFCYLVIIR TLLQARNFERNXXXX 263
+ ++E + + + +++ GF +PL+ M FCY I++TL+QA+N +R+
Sbjct: 343 DVCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFMIFCYTFIVKTLVQAQNSKRHK AIR 402

Query: 264 XXXXXXXXXXXXQLPYNGV VLAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNP 323
Q+P+N +VL T AN + +C+ K + VT LA + CC+NP
Sbjct: 403 VIIAVVLVFLACQIPH N-MVLLVTAANLGKMNRSQCSEKLIGYTKTVTEVLAFLHCCLNP 461

Query: 324 FLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHRRSSMSVEAETTTT 375
LYAFIG KFRN K+ KDL C+ ++ SC R S ++ +T+ T